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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 A24194 LOCUS DEFINITION ACCESSION		J 44 ⊓	n N	10	ωα	37 3	n Non H	w w	2	0 4	000	20	44 TU	ωĸ	, <b>⊢</b> (	o	00 ~	1 0/	44 TJ	ωĸ	11 5	O V	,	ע 1 ס	ωή	ωd	22 -		Result No. S
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IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
                                             GTTCTTGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCT
                                                                                                              AAAATTTAGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAA
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/db_xref="G1:904405"
/db_xref="GOA:P05117"
/db_xref="SWISS-PROT:P05117"
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/mol_type="unassigned DNA"
/db_xref="taxon:4081"
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TA-	CAAAAGTTTGACGATTGTACTTTTTAATGTACAAAAATAATAAATGGTT	1561	Дb
ATTTATAT 1620	GTCAAAAGTTTGACGATTGTACTTTTTAATGTACAAAAAATAATAAATGGTT		Qy
ATTTTCTA 1560	TTATTATTAATATGTACGGATTGAAGTTTTAATAAGACTACTATGTATTTCT	1501	Дb
- 123	ATTATTAATATGTACGGATTGAAGTTTTAATAAGACTACTATGTATTTCT		γQ
  TGAATAA 1500	TCAATATATAGCAGATATGATATATCACAATAAACAAATCTATATCTATGTAT	1441	Дb
TGAATA	TCAATATATAGCAGATATGATATATCACAATAAACAAATCTATATCTATGTAT	1441	Ϋ́O
ATAGATCT 1440	CACTAGAAATTTCAGAGGATGAAGCTCTTTTGTATAATTTAATTTATACTA	1381	da
TAG	CACTAGAAATTTCAGAGGATGAAGCTCTTTTGTATAATTATTTAT	i	VQ.
CTGCACTT 1380	AGGCTACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACA	1321	Dβ
CIGCACI	AGGCTACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACA	į.,	VQ VQ
ACCATCAG 1320	CATGTGAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAGTGGAAAACC	1261	Дb
CATCA	CATGTGAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAGTG	1261	γQ
ACAAACTTTC 1260	ATATCAAGGGCACAAGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCAC	1201	ДD
1111	ATATCAAGGGCACAAGTGCAACAAAGGTGGCCATAAAATTTGGATTGCAGC	1201	γQ
	GAGTTGAACCATGTATACAACAGTTTTCAGCAGTTCAAGTGAAAAAAT	1141	Db
12	GAGTTGAACCATGTATACAACAGTTTTCAGCAGTTCAAGTGAAAAAT	1141	χ <sub>ζ</sub>
TTGTGATC 1140	TGAATGTGGAAATGCAAGACGTTAAGTATCCCATAATTATAGACCAAAACTATTGT	1081	Дb
-GAT	TGAATGTGGAAATGCAAGACGTTAAGTATCCCCATAATTATAGA	1081	Ş
CAAATTTC 1080	ATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACA	1021	DЬ
CAAATTTC 1080	ATGGAGTTAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACA	1021	Ş
GCCGAAA 10	ATTCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTATCGC	961	DЬ
- ଜୁ	ATTCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTATCGC	961	Ş
	CCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCT	901	Дb
ATCTGGAA 960	. CCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCT	901	Ş
TGTGCAGG 900	CTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAAT	841	Db
ADDLE	. CTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTC	841	8
 ATCTGATA 840	AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAAT	781	Db
ATCTGAT	AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAAT	781	γQ
  TCAGCAA 780	TCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAATGCTTCA	721	da
٠ <u>۵</u>	TCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTTGAT	721	δ
  CAAATTCATA 720	GGAATTGCAAAAATTTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAI		뫄
ICAT	. GGAATTGCAAAAATTTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAA	661	γQ

DNA

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PAT 03-SEP-2003

Db 1  RESULT 3 AL5981 LOCUS LEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	0y 1	0V 1	Qy 1	Qy 1 Db 1	Qy 1	Qy 1 Db 1	Qy 1 Db 1	Qy 1 Db 1	Qy 1 Db 1	Db 89	Db Qy	Db	מם
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AAAAAAA 163 AAAAAAA 163 AAAAAAA 163 AAAAAAA for I:490039 In esculentu Viridiplant Va; Magnoli Lto 1621)		TAGCAGATA           TAGCAGATA	ATTTCAGAGGAT           ATTTCAGAGGAT	TGCAAAAATGTC           TGCAAAAATGTC	IGGAATTATAATGO            IGGAATTATAATGO	GGCACAAGTGC           GGCACAAGTGC	CATGTATACAA            CATGTATACAA	GAAATGCAAGAC            GAAATGCAAGAC	AGGATCAAGAC           aggatcaagac	GCTTATGTO           GCTTATGTO	ATTACTTGTGGTCCAGGTC	TGGAACAGGTGATO           TGGAACAGGTGATO	
l621 b lygala lygala (tomat ; Stre hyta; ales;	TIGAAGTTTTAAT TIGAAGTTTTAATGTA ACTTTTTAATGTA	ATATCAC         ATATCAC	AAGCTCTTTG           AAGCTCTTTTG	CATTTTAACAATG             CATTTTAACAATG	ETATAATGGAGAATATAAATTT 	CAAAGGTGGCC           CAAAGGTGGCC	;aacagttttcagcag            ;aacagttttcagcag	GTTAAGTATCCCA           GTTAAGTATCCCA	GGCAGGGAGGAT             GGCAGGGAGGAT	ATGTTACTG	ATGGTA	GATTGTATTTCAA              GATTGTATTTCAA	
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                                    ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTTGGAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The predicted N-terminal AA sequence of PG-2a occurs at AA72. Since the ATG at bp 51 codes for the only inframe methionine preceding the N-terminal sequence of PG-2a, it is probable that the mRNA is translated with a 71AA pre-sequence that is subsequently cleaved to give a 41,828D mature protein.

Data kindly reviewed (22-APR-1987) by D. Grierson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3786135
The pred
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grierson, D., Tucker, G.A., Keen, J., Ray, J., Bir Sequencing and identification of a cDNA clone
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Nucleic Acids Res.
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erson,D., Tucker,G.A.,
                                                                                                                                                                                            /db_xref="GOA:P05117"
/db_xref="GOA:P05117"
/db_xref="SWISS-PROT:P05117"
/db_xref="SWISS-PROT:P05117"
/ranslation="MV1QRNS1LLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEF
AHDFQAYLSXLISUNIUNIUKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEA
CSSRIPVQFVVFKNNYLLKQIIFSGFCRSSISVKIFGSLEASSKISDYKDRRIWIAF
BSVQNLVVGGGGTINGNGQVWAPSSCKINKSLFCRDAPTALTFWNCKNLKVNNLKSKN
AQQIHIKFESCTNVVASNLMINASAKSDHTDGVHVSNUTQYIQISDTIIGTGDDCISIV
GSQNVQATUTTGCGPGHGISIGSLGSGANSAYVSNVTVNEAKIIGAENGVRIKTWGGG
SGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATK
VAIKFDCSTNFPCEGIIMENINLVGESGKF8EATCKNVHFNNAEHVTPHCTSLEISED
                                                                                                       615
                                                                                                                                                                       264.
                                                                                                                                     /product="mature 51. .263
                                                                      /note="pot.
768. .776
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                                        /note="pot.
906. .914
                                                                                                       /note="put.
615. .623
                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA28254.1"
/db_xref="GI:19292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="fruit ripe"
51. .1424
                                                                                                                                                                                                                                                                                                                                                                                                                          note="unnamed protein product;
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                                                     N-glycosylation site"
                                                                                     N-glycosylation
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CCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCTTAGGATCTGGAA
                                                   CTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGG
                                                                      CTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAAIGTGCAGG
                                                                                                                                       AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAAATATATTCAAATATCTGATA
                                                                                                                                                                                                                                             GGAATTGCAAAAATTTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAACAAATTCATA
                                                                                                                                                                                                                                                                            GGAATTGCAAAAATTTGAAAGTGAATAATCTAAAGAGTAAAAATGCACAACAAATTCATA
                                                                                                                                                                                                                                                                                                                               GTTCTTGCAAAATAAATAAATCACTGCCATGCAGGATGCACCAACGGCCTTAACCTTCT
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                                                                                                                   AGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATA
                                                                                                                                                                               TCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAATGCTTCAGCAA
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1621
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Pred. No. 6.4e-244;
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1859845
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 1617)
                                            Rogers,H.J., Allen,R.L., Hamilton,W.D. and Pollen specific cDNA clones from Zea mays Biochim. Biophys. Acta 1089 (3), 411-413
                                                                                                                                      Sheehy,R.E., Pearson,J., Brady,C.J. and Hiatt,W.R. Molecular characterization of tomato fruit polygal Mol. Gen. Genet. 208, 30-36 (1987)
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/db_xref="G1:19298"
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Hiatt, W.R., Sheehy.R.E., Shewmaker, Pg gene and its use in plants
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Saiprasad, G.V.S.
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Isolation, cloning and characterization of polygalacturonase from ripening papaya fruit (Carica papaya cv. Singapore PP-1)
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/protein_id="CAD44275.1"
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/gene="pg:	CDS	DG GENERAL GEN	OV {
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,	FEATURES source	589; Conservative 0; Mismatches 10; Indels 3; Gaps	Matches
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10794531 2 (bases 1 to 1541 Atkinson, R.G.	PUBMED REFERENCE AUTHORS	APTALTEWNCKMLKVNNLKSKNAQQIHIKEESCTWVVASNLMINASAKSPNTDGVHVS NTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHG"	ORIGIN
fruit softening and ethy Plant Mol. Biol. 42 (2), 20252524	JOURNAL	/db_xref="GI:34481843" /translation="BQAWNEACSSRTPVQFVVPXNKNYLLKQITFSGPCRSSISEKIF GSLEASSKISDYKDRRLLDCLLKSVQNLVVEGGGTINGNGQVVWWPSSCKINKSLPCRD	
Atkinson, R.G. Polygalacturonase gene	TITLE	<pre>/product="putative polygalacturonase" /protein_id="CAD44521.1"</pre>	
	REFERENCE	/gene="pg" /codon_start=2 /evidence=experimental	
7.		. ^ ~	CDS
Actinidia chinensis Actinidia chinensis	SOURCE		gene
AF152758.1 GI:7959982	VERSION KEYWORDS	/cultivar="Arka vikas" /db_xref="taxon:4081"	
complete cds. AF152758	ACCESSION	/organism="Lycopersicon esculentum" /mol_type="mRNA"	
AF152758 Actinidia chinensis	LOCUS	н	FEATURES sour
	RESULT 10 AF152758	AL Submitted (19-A0G-2002) Saiprasad G.V.S., Biotechnology, Indian Institute of Horticultural Research, IIHR, Hessaraghatta Lake post, Bangalore, Karnataka, INDIA	JOURNAL
17		Direct Submission	TITLE
932 IA 933 601 TA 602	당		REFERENCE AUTHORS
		from fruit tissue of Lycopersicum esculentum cv. Arka vikas	TANGITOT
872 AATTGTTTCTGGATCTCAAAA [	B 29	RCB I solprasad, G.V.S.  Isolation, Cloning and characterization of polygalacturonase gene	AUTHORS TITLE
81 AAATACTC			
812 AAATACTCAATATATTCAAAT	Qy		ORGANISM
421 TTCAAATTTGATGATCAATG	ממ	pg gene; pol	KEYWORDS SOURCE
752 TTCAAATTTGATGATCAATGCT	Qy	z	ACCESSION VERSION
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692 AAAGAGTAAAAATGCACAACA	ν,	LES505947	LESSOS947
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		41 TGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATGGTA	DЪ
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572 CAATGGCAATGGACAAGTATGG	Q		DЪ

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ygalacturonase A"
AAF77160.1"
7959983"
"MALQRHFFQFVIITLLIPSFILGYTSAVHEDPPHDYHLEEYGYD
NDFGSSMSHENGIFGLRKVDYGMDRVLDASKTVNVDDFGAKGDGS
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ew Zealand
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one CkPGA-3 polygalacturonase A (PGA) mRNA,
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                                                                                        GGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAG
                                                                                                                                      GTGGTGAATGGAGCTAAGCTTTGTGGAACTACAAATGGAGTCAGGATTAAGACATGGCAG
                                                                                                                                                                               ACTGTAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAG
                                                                                                                                                                                                                               CATGGAATCAGTATTGGAAGCTTAGGATATGGGAATTCAGAGGCTCATGTATCAGATGTG
                                                                                                                                                                                                                                                              CATGGTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTT
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                                             GGGGGATCTGGAAGTGCAAGCATCAAATTTCAGAATGTGGAAATGCATAATGTGGAA
                                                                                                                                                                                                                                                                                                                        ATTTCAATTGTAAGCGGGGGTCAGAAGGTGCGGGTCAATGATATAACCTGTGGACCAGGT
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Query Match Best Local S Matches 815

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3 (bases 1 to 1595)
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Vitis vinifera
AY043233
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Submitted (02-JUL-2001)
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Fincher, G.B.
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Nunan, K.J., Davies, C.,
Expression patterns of
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FENVQNLAVQGGGTINGNGKTWWENSCKVNYDLPCKGAPTALTFYNCKNLAVKNLKIQ
NAQQMHVSFSKCVGVQASGLTITAPGNSPNTDOSTHVSYTKIIQISSSVIGTGDDCISI
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KEAISLDCSAKFPCQGILLRDIDIKVGGGKAAKAVCSNARVTVMGDVSPNCA."
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/cultivar="Shiraz"
                                                                                                                                                                                                                                                                                                                                organism="Vitis vinifera"
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                         TTAACAATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTTCAGAGGATGAAG 1404
                                                          ACATTGATATAAAAGTTGGAGGAGGAAAGGCAGCCAAAGCTGTATGCAGCAATGCCAGAG 1351
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Lycopersicon esculentum
Lycopersicon esculentum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Bird,C.R., Smith,C.J., Ray,J.A., Moureau,P., Bevan,M.W.,
Hughes,S., Morris,P.C., Grierson,D. and Schuch,W.
The tomato polygalacturonase gene and ripening-specific
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6785 CAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCA
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                                                                                                                   Bird, C.R., Smith, C.J., Ray, J.A., Moureau, P., Bevan, M.W., Bird, A.S., Hughes, S., Morris, P.C., Grierson, D. and Schuch, W.
The tomato polygalacturonase gene and ripening-specific expression
                                                                                                                                                                                Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
[bases 1 to 7456]
                                            in transgenic plants
Plant Mol. Biol. 11, 651-662 (1988)
Plant Mol. Biol. 11, 651-662 (1988)
L. 7456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGCTCTTTTGTATAATTTAATTTATTATAGATCTTCAATATATAGACAGATATGA
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/note="polygalacturonase
6139. .6255
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putative"
5602. .5710
  /organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
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/number=9
                                                                                                                                                                                                                                                                                                                                                                   7456 bp DNA linear PI for cell wall degrading polygalacturonase.
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Pred. No. 5.3e-63;
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Matches 462
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CAAT_signal
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1161 CAGTITICAGCAGTICAAGTIGAAAAATITIGGGIGTATGAGAAATATICAAGGGCACAAGTIGCA 1220
                                                            tch 28.2%; S
al Similarity 100.0%;
462; Conservative 0;
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5711.
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6256. .678
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/db_xref="SMISS-0RO]: D05117"
/translation="mylqrnstlllilipassistcrsnviddnlekgvydnillegeb
Aldpqaylsylskniesnnnidkydkngikvinvlspgakgdgktydniafeqamnea
CSSRTBYQFVVPKNKNYLLKQITFSGPCRSSISVKLEGSLEASSKISDYKDRRLMIAF
DSVQNLVVGGGGTINGNGQVMMPSSCKINKSLPCRDAPTALTFMVCKNLKVNNLKSKN
AQQIHIKFESCTNVVASNLMIMASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIV
SGSQNVQATNITGGPGGISIGSLGSGSSEAVSNUTVVSNTIKTGGG
GGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEDCIQDFSAVQVKTVVTENIKGTSATK
VAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHCTSLEISED
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/db xref="taxon:4081"
/clone_lib="lambda EMBL:
877. .904
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1758. .2
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6788. .7244
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4260. .446
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3717. .4259
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2416. .25
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4260. .4467,4567. .4648,5602. .5710,6139. .6255,6788.
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/product="polygalacturonase"
/protein_id="CAA32235.1"
/db_xref="GI:295813"
/db_xref="GI:295813"
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                                                            Score 462; DB 8; ]; Pred. No. 5.3e-63; 0; Mismatches 0;
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                                                                                                  Length 7456;
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KEYWORDS SOURCE ORGANISM

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FEATURES

JOURNAL TITLE DEFINITION ACCESSION VERSION

Tomato gene for cel X14074 X14074.1 GI:19305 polygalacturonase.

RESULT 13

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AK117942
                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Scienc Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:msekigsc.riken.go.jp, URL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9625, Fax:81-45-503-9586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK117942.

AK117942.1 GI:26450945

FLI CDNA, CAP trapper,
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                   as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). CDNA cleaved with BamHI
and KhoI was ligated to modified Lambda FLC-1-E vector (Carninci
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (2002)

2 (bases 1 to 1600)

Seki,M., Tida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J.,
Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK117942 1600 bp mRNA linear PLN 06-Arabidopsis thaliana At3g57510 mRNA for putative endo-polygalacturonase, complete cds, clone: RAFL19-13-H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                             An Arabidopsis full-length cDNA library was constructed essentially
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakajima,M., Enju,A., Kamiya,A., Narusaka,M.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thaliana full-length cDNA
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                                                                                                                                     visit our web site (http://pfgweb.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iida, K.,
/organism="Arabidopsis
/mol_type="mRNA"
/cultivar="Columbia"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satou, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakurai, T.,
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                          GTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTG
                                                                                                                                                                                                                           CAAATACTCAATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTTGAAAGTGAATAATC
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  GGATCAGCATTGGGGAGCTTGGGGGGACGACAATTCGAAAGCTTATGTCTCGGGAATTAATG
                                                                                             CCATTGAGGATGGAACGCAAAATCTTCAAATCTTTGATTTAACTTGCGGCCCCCGGTCACG
                                                                                                                            CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG
                                                                                                                                                                                     CTAATACTCAAAACATTCGAGTCTCCAACTCAGATATCGGAACAGGTGATGATTGTATAT
                                                                                                                                                                                                                                                                                                                   CTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTAT
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QIPDLTGPGHGISIGSLGDDNSKAYVSGINVDGKFSBSDNGVRIKTYQGGSGTAKN
IKPQNIRMENVKNPIIIDDYYCDKOKCEDQESAVQVKNVVYKNISGTSATDVAITLNC
SEKYPCQGIVLENVKIKGGTASCKNANVKNQGTVSPKCS"
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KLNNDDVLSLISSDETTLEASTVSVSNFGAKGDKTDDTQAFKAWKKACSTNGVTT
FLVPKGKTYLLKSTPÆFGPCKSLRNFQLLGTLASTTKASDYKDKUHMLILEDVNNLSI
DGGSTGIINGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQI
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/db_xref="G1:26450946"
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/codon_start=1
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/chromosome="3"
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Query Match Best Local S Matches 720	FEATURES sourc	JOURNAL	ORGANISM REFERENCE AUTHORS	RESULT 15 AX412563 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE	Qy Db	Db	QQ da	Qy Db	Qy Db	Db dy	dg Qy	Qy Db	QY dd	Qy Db
Y Match 27.2%; Score 445.2; DB 6; Length 1296; Local Similarity 64.7%; Pred. No. 3.4e-60; hes 720; Conservative 0; Mismatches 368; Indels 24; Gaps 3;	ro	infection of which are infection of which are infection of which are infection with the patient wo 0222675-A 327 21-MAR-2002; Syngenta Participations AG (CH); UNIVER: CHAPEL HILL (US); Glazebrook, Jan (US)	SM Arabidopsis thaliana  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e Spermatophyta; Magnoliophyta; eudicotyledons; core e Spermatophyta; Magnoliophyta; Brassicaceae; Arab  E 1 Collagebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zh S Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T.	AX412563 AX412563 Sequence 327 from Patent WO02226 AX412563 AX412563.1 GI:21445021	1531 AATA 1534         1535 CATA 1538	1471 TAAACAAATCTATATCTATGTATTGAATAATTATTAATATGTACGGATTGAAGTTTT 1530	1411 TGTATAATTATTAATTTATACTATAGATCTTCAATATATAGCAGAGATATGATATATACACAA 1470	1351 ATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTTCAGAGGATGAAGCTCTTT 1410	1291 ATTTAGTAGGGAAAACTGGAAAAACCATCAGAGGCTACGTGCAAAAATGTCCATTTTAACA 1350 	1231 CCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATAA 1290	1171 CAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGGTGG 1230	TATACAACAGTTTTCAG 	0-0 1-1	991 TAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAG 1050 
Q Db	ДЬ Оу ДЬ	Qy Qy	Db Db	לם עם לם עם	8 B 8	y da Y	Ωy	Db Qy	Db Qy	Qy da	g dy	Db Qy	Qy	Qy
1291 ATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGCTACGTGCAAAAATGTCCATTTTAACA 1350	1100 CAGTGCAAGTGAAAACGTTGTGTACAAGAACATATCTGGTACGAGCGCTACGGATGTGG 1159  1231 CCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATAA 1290	1111 CCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCAG 1170	923 TGGATGGTGCTAAGTTCTCTGAGAGTGACAATGGAGTTAAGGACTTAATCAGGGAG 982 1051 GATCTGGACAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTATC 1110 111111111111111111111111111111111		811 CAPATACTCARATATTCAPATATCTGATACTATTATTGGAPCAGGTGATGATTGTATTT 870	CTTCAAATTTGATGATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTAT  CTTCAAATTTGATGATCACTGCTTCAGCAAAGAGCCCAACACAGATGGTATCCATATCA  TTAGTAATGTTGAGATCACTGCTCCGGGCGATAGTCCCAACACAGATGGTATCCATATCA	691 TAAAGAGTAAAAATGCACAACAAATTCAAATTTGAAGTCATGCACTAATGTTGTAG 750	631 GCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATAATC 690	571 TCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCAAAATAAAT	517 TITGGATTGCTTTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGAGGAACTA 570	457 TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGC 516	397 ACAAGAATTATCTTCTAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG 456	337 AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAA 396 	277 TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAACATATGATAATATTGCATTTG 336 

Db 1265 ATCAAGGCACCGTTTCTCCTAAATGCTCTTAA 1296
Search completed: July 27, 2004, 01:30:44
Job time: 6486 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Abb91537
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Aab48338
Abr43936
                                                                               Aar48674
Aae00422
                                                                                                                                           Aag41324
Abb92704
                                                                                                 Aay42649
                                                                                                         Aaw04268
                                                                                                                          Aag413
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                                                                                                                                                                     Abb92243
                                                                                                                                                                                                                                  Description
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                   Brassica
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AAP80299
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DT 20-N
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DE Poly
XX
                           Best Local Similarity
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polygalacturonase (PG) is encoded by plasmid clone pTOM6 which is used to produce antisense mRNA (with an inverted sequence to that of PG mRNA) which is inserted into a vector used to transform plants which thereafter have altered ripening properties. The inverted sequence and the PG mRNA form a double-stranded structure which inhibits ex- pression of the PG mRNA. See also AAN80488. (Updated on 25-MAR-2003 to correct PA
                          Sequence
                                                                                                                                                                                                     (ICIL )
                                                                                                                Disclosure;
                                                                                                                              Recombinant DNA comprising promoter and terminator sequences - useful plants for altering ripening properties esp. in tomatoes.
                                                                                                                                                                                                                                                                                 EP271988-A.
                                            field.)
                                                                                                                                                           WPI; 1988-169271/25.
N-PSDB; AAN80487.
                                                                                                                                                                                     Bridges IG,
                                                                                                                                                                                                                                                 06-NOV-1987;
                                                                                                                                                                                                                                                                  22-JUN-1988
                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                     Fruit ripening;
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20-NOV-1990
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                                                                                                              Page ?; 22pp; English
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(first entry)
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                                                                                                                                                                                                                                                                                                                     polygalacturonase;
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(100.0%;
(100.0%;)
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AAM51693
AAM51691
AAB51691
ABB90812
ABB92113
AAB92113
AAB92116
AAB93472
AAG05118
ABB93472
AAG09145
AAB92116
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ADC34914
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AAY25667
ADC34915
AAR53690
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AAR93599
Score 2390; DB 1;
Pred. No. 7.3e-194;
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       Length 457;
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Abb93472
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Aay25666
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Abb90812
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Adc34915
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Result No.

Score

Query Match

Length

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AAP94619 AAR32107

AAP80299

ABB91108 ABB91537 AAW42122

AAG52346 AAG52347

AAW04346 ABB91377

2390 2390 2390 2390 23390 23390 23380 23380 11127 11127 11127 11127 1115.5 1115.5 1115.5 845.5 845.5 845.5 787.5

AAY42649 AAR48674

AAE00422 ABB91673

AAG41325 ABB92075 AAW04268

100.0 100.0 100.0 100.0 97.8 49.6 47.2 47.2 46.8

ABB92243 AAW98178 AAG41324

ABR43936 AAB48338

ABB92704 AAG41323

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Database

A\_Geneseq\_29Jan04:\*

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geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003abs:\*

geneseqp2004s:\*

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB Maximum DB

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length: 0 length: 2000000000

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Scoring table:

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Japanese Japonicum Japanese Cedar all Cedar

Title: Perfect score:

US-10-018-604-2 2390 1 MVIQRNSILLLIII

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on:

July 21,

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21-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP94619 standard;
                                                                                                                                                                                                WPI; 1989-053640/07.
N-PSDB; AAN91112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polygalacturonase (PG) cDNA gene product.
  cDNA of gene may act as a probe of modulating the production of
                                                                      Disclosure; Page; 8pp; English.
                                                                                                                         Tomato polygalacturonase gene - ucells or directing expression of
                                                                                                                                                                                                                                                                       Hiatt WR,
                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1986;
17-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JAN-1987;
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                                                                                                                                                                                                                                                                                                                       (CALJ ) CALGENE INC
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86US-00920574.
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       to the PG and
                                                                                                                         used for modulating expression f heterologous peptide(s).
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       genomic sequence, provides a means acts as a source of the transit
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Best Local Similarity 100.0%;
Matches 457; Conservative
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25-MAR-2003
05-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 457 AA;
                                                                                                                                                                                             polygalacturonase; PG; pectin esterase; PE; expression regulation; fruit softening enzymes; flowering plants; fruiting plants; antisense RNA.
                                                                                                                                                                                                                                                                                                                                             AAR33107 standard;
                                                                                                                                                                                                                                              Polygalacturonase.
          Bridges IG,
                                                                                              06-NOV-1987;
                                                                                                                     17-MAR-1993
                                                                                                                                              EP532060-A1.
                                                                                                                                                                      Lycopersicon esculentum
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                                (ICIL ) IMPERIAL CHEM IND PLC. (ZENE ) ZENECA LTD.
                                                                      11-NOV-1986;
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            Schuch WW
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Pred. No. 7.3e-194;
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                 Lycopersicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA for flowering and fruiting plants e.g. tomatoes ripening control - comprises base sequence for transcription contg. inverted sequence of bases complementary to bases in anti sense ribonucleic acid encoding softening enzymes, or gene expression regulation.
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                                         ln; pectin methylesterase; PME; polygalacturonase; PG; tomato; pTON
product; yogurt; milk; fruit juice; whey drink; de-esterification.
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Pred. No. 7.3e-194;
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Matches 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying pectin, for foodstuffs preparation, involves transforming host having pectin methylesterase (PME) and polygalacturonase (PG) activity by silencing PG activity, to increase PME to PG ratio.
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KPSEATCKNVHFNNAEHVTPHCTSLEISEDEALLYNY
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100.0%; Pred. No. 7.3e-194;
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KPSEATCKNVHFNNAEHVTPHCTSLEISEDEALLYNY

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                                                                                                                                                                                                                                                                                               Query Match
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Matches 452
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to forming an ester or amide bond between monomeric or polymeric ester or its acid or salt and monomeric or polymeric alcohol or amine by treating the ester or its acid or salt with a plant pectin transester synthase in the presence of alcohol or amine under conditions to form ester or amide bond. The method is useful for forming an ester or amide bond between monomeric or polymeric ester or its acid or salt (e.g. homogalacturonan) and monomeric or polymeric alcohol or amine. It is useful for producing pectin-based polymers e.g., xyloglucan or D- or L-polylysine, useful for the slow release of compounds in the body e.g., heparin with anticoagulant or other pharmaceutical properties. The present sequence represents an endopolygalacturonase enzyme from tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Formation of ester or amide bond between ester and alcohol involves treating the ester or its acid or salt with plant transester synthase in the presence of alcohol or amine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; pectin transester synthase; xyloglucan; polylysine; heparin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticoagulant;
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452; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein;
                                                                                                                                           LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQV
                                                                                                                                                                              SNINIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                                                                                                                                 SNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                   WWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMIN 240
                                                                                                                                                                                                                                                      MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIE
                             ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
                                                                                                                                                                                                                                      MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIE
 ASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSL
                                                            WWPSSCKINKSI
                                                                                                                    LKQITFSVDKNSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQV
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Pred. No. 1.7e-189;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbicidal; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidally active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016)
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                                                                                                                                                                                                                                                                                                              Sequence
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                                                NNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL 121
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                                                                                                      ILLLIIIFASSISTCRSNV---IDDNLFKQ---VYDNILEQEFAHDFQAYLSYLSKNIES
  KNRHGYAPRSSPRSFNVNTFGAKANGND-DSKAFMKAWEAACSSTGIVYIVAPKNRDYML
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Pred. No. 1.2e-91;
6; Mismatches 121
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KQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVW

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RESULT 7
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seed production. The promoter is used to drive expression of a further nucleic acid sequence that results in prevention or reduction of anther dehiscence. For example, expression of the RNase barnase causes cell ablation, while expression of a plant hormone alters the developmental fate of a cell. Plants are produced that have phenotypically normal pollen grains, within phenotypically normal anthers, but in which the anthers do not dehisce and thus do not release the pollen grains. The system allows the female to be multiplied with the artificial male sterility gene in the homozygous state, since the female plant produces viable pollen. The system is suited to crops which have high seed multiplication, large amounts of pollen, and/or separate male and femal inflorescences. These factors allow for easy collection of pollen from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESJ2A gene;
transgenic [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOG-)
                                                                                                                                                                                                                                                                                                                                                     protein is encoded by the ESJ2A gene (see AAX25011) of Arabidops:
iana. The invention relates to the use of the ESJ2A promoter to
see dehiscence and to create male sterile plants for use in hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOGEMMA
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DVSKASCSNVKLDTRGNVSPLCT
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Best Local :
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-dehiscing anthers, facile self-pollination and the minimisation of the area of plants that have to be self-pollinated manually. Such an ideal crop is the monocot maize, but the system is also applicable to e.g. wheat, barley, rice, fodder grass, banana, palm, orchid, tulip, lily, melon, cucumber, tomato, pepper and willow. It is also useful the avoidance or reduction of pollen allergens and may be effective the control of asthma caused by pollen release
                                                                                                                                                                                                                                                    EP1033405-A2
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                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                 termination
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                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 431
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99US-0123180P.
99US-0123548P.
99US-0125788P.
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                                                                                                                                                                                                                                                                                                                                                                                            mapping; gene expression control;
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promoter;
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-JUL-1	2-JUL-19	8-JUL-19	112	1-JUL-19	0-JUN-19	9-JUN-19	9-JUN-19	3 - JUN - 19	3-JUN-19	2-JUN-19	1 - JUN - 1 S	8-JUN-19	8-JUN-19	8-JUN-19	B - TTTN - 1 C	O TIN 1	ST-NOC-B	T-NOC-B	NOC-B	8-JUN-19	8-JUN-19	-JUN-19		-JUN-19	-JUN-19	-JUN-19	-JUN-19	8-JUN-19	7-JUN-19	4-JUN-19	3-JUN-19	1-JUN-19	8-MAY-19	7-MAY-10	5-MAY-10	A-MAY-10	1 - MAY - 1 0	19-MAY-1999;	B-MAY-19	4-MAY-19	4-MAY-19			MAY-19	7-MAY-19	6-MAY-19	6-MAY-19	5-MAY-10	-MAY-10	0-APR-10	30-ADR-1999;	- APK-10	4	, <u>L</u>	1	-APR-19	-APR-19	125	R-19	R-19	39-MAB-1999
99US-0143624P. 99US-0144005P. 99US-0144085P.		50,00	95	-01	5 6	-01		25	01	01	25	201	-01	0	0 1	9 1	2 5	2 -	- L	01	-	0	-01	-01	-01	-01	-01	-01	-01	-01	-01	01	-01	01	01	01.	01	01.	01	T 0	01	-01	-01	-01:	-01	01	01	-01	01:	01:	01	0	-01	20	01	01	-01	TO	-01:	-01	2 1
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PR 05-0CT-1999; PR 07-0CT-1999; PR 07-0CT-1999;	29-SEP-1999	R 24-SEP-1999	R 22-SEP-1999 R 23-SEP-1999	R 20~SEP-1999	15-SEP-1999	R 13-SEP-1999	10-SEP-1999	01-SEP-1999	31-AUG-1999	AUG-1999	AUG-1999 AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AIIG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-1999	AUG-199	10-AUG-1999	09-AUG-1999	09-AUG-1999	06-AUG-1999	06-AUG-1999	05-AUG-1999	05-AUG-199	04-AUG-1999	04-AUG-1999	03-AUG-1999	02-AIG-1999	02-AUG-1999	. 28-JUL-1999	27-JUL-1999	27-JUL-199	27-JUL-1999	26-JUL-1999	23-JUL-1999	JUL-199	JUL-199	JUL-199	JUL-199	JUL-199	JUL-199	21-JUL-199	21-,7111-199	21	20 TIT 100	20-JUL-199	19-JUL-199	19-JUL-199	19-JUL-199	19-JUL-199	19-JUL-199	66T-TOP-6T	19777

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Best Local Sim
Matches 223;
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 ABB92704;
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                                                                                    KIKG-
                                                                                                         NLVGESGKPSEATCKNVHFNNAEHVTPHCT
                                                                                                                                                       PIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENI
                                                                                                                                                                                GISIGSLGDDNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKN
                                                                                                                                                                                                    GISIGSIGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                                                                                                                                                                               VSNVEITAPGDSPNTDGIHITNTQNIRVSNSDIGTGDDCISIEDGTQNLQIFDLTCGPGH
                                                                                                                                                                                                                                                 ASNLMINASAKSPNTDGVHVSNTQVIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGH
                                                                                                                                                                                                                                                                                                   INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                                                                                                                                                                GKTYLLKSTRFRGPCKSLRNFQILGTLSÅSTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                                                                                                                                                                                                                                                                              NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
                                                                                                                                                                                                                                                                                                                                                                                  ETTLEAS-----
                                                                                                                                                                                                                                                                                                                                                                                                    SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SILLLIIIFASSISTCRSNVID------DNLFKQVYDNILEQEFAHDFQAYLSYL
                                                                                                                                PIIIDQDYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV
                                                                                                                                                                                                                                                                                INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL
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99US-015964P

99US-0160741P

99US-0160767P

99US-0160770P

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99US-0159331P.
                                                                                   -GTASCKNANVKNQGTVSPKCS
                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.2%;
49.6%;
                                                                                                                                                                                                                                                                                                                                                                               --TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
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                       431
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Pred. No. 9
                       AA
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                                                                                  431
                                                                                                          443
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9.4e-87;
nes 116;
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Best Local Sim
Matches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying modulators.
herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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PIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENI
                                                 GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                                                                                                                                                                                  NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
                                                                                                                                                                                                                                                                                     SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                                                                                                                                                                                    SILLLIIFASSISTCRSNVID-----
                                GISIGSLGDDNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKN
                                                                                       VSNVE TTÄPGDSPNTDGTHITNTQNIRVSNSDIGTGDDCTSTEDGTQNLQIFDLTCGPGH
                                                                                                                  ASNIMINĀSĀKSPNTDGVHVSŅTQYIQISDTIIGTGDDCISIVSGSQŅVQATNITCGPGH
                                                                                                                                                INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVB
                                                                                                                                                                          INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                                       GKTYLLKSTRERGPCKSLRNEQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                                                                                                                                                                                                 ETTLEAS-
                                                                                                                                                                                                                                                                                                                       AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL-----SLISSD
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 1915;
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49.6%;
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                                                                                                                                                                                                                                                               -TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
                                                                                                                                                                                                                                                                                                                                                                                          Score 1127; DB 5;
Pred. No. 9.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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                                                                                                                                                                                                                                                                                                                                                  ----DNLFKQVYDNILEQEFAHDFQAYLSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing;
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348

PITIDODYCDK-DKCEDQESAVQVKNVVYKNISGTSATDVAITLNCSEKYPCQGIVLENV

347

353

287 293 227 233 167 107 115 59 55

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ARESULT 10
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AXX AAG41
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PR 25-M3
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25-FBB-1999
05-MAR-1999
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06-MAY-1999
07-MAY-1999
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16-AUG-1999;
17-AUG-1999;
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hes 223;
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                 SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                               Conservative
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99US-01513303P
99US-0153363P
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99US-0149722P.
                                                                                                  47.2%; 5
49.6%; Pred
71;
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Pred. No. 1e-86;
1; Mismatches 116;
 Length
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
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cransgenic

plant;

antisense

Oilseed

rape

pod polygalacturonase

(revised) (first en seed

entry)

AAW04268; 16-OCT-2003 14-DEC-1996

> 403 418 345 358 285 298 225 238 172

Polygalacturonase; seed pod; dehiscence;

shatter; oilseed

rape

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Best Local Sim
Matches 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                                                                           SGKPSEATCKNVHFNNAEHVTPHCTS
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Best Local
              AAY42649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A polygalacturonase (PG) (AAW04248) of oilseed rape cv. Rafal seed pods is useful for controlling dehiscence. Manipulation of the enzyme's activity can influence the timing of dehiscence. A cDNA clone (AAT33994) coding for the PG was isolated from a cDNA library of the rape seed pod dehiscence zone. PG nucleic acids (partic. antisense) can be used to regulate dehiscence in crop plants. (Updated on 16-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1;
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              standard;
                                                                                                                                       QNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMFNCSVKYPCQGIVLENVNIKG-
                                                                                                                                                              QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                                                           SLGDDNSKÄYVSGINVDGÄTLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPIIID
                                                                                                                                                                                                                   SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
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                                                                                                                                                                                                                                                                                                                                                                                         KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433
                                                                                                           SGKPSEATCKNVHFNNAEHVTPHC 442
                                                                                                                                                                                                                                                                             INASAKSPNIDGVHVSNIQYIQISDIIIGIGDDCISIVSGSQNVQATNIICGPGHGISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIFLCVLLMLACCQALSSNVDDGYGHEDGSFET--DSLIKLNNDDDVLTLKSSDRPTTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES
                                                                                                                                                                                                                                                   ITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGISIG
                                                                                                                                                                                                                                                                                                       KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seed pod dehiscence - using polygalacturonase or nucleic derived from polygalacturonase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                   -GKASCKNVNVKDKGTVSPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coupe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SA,
                                                                                                                                                                                                                                                                                                                                                                                                                      ---TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLIPKGKTYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
              433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1103; DB 2;
Pred. No. 1e~84;
0; Mismatches 125;
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                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod of an another in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The pressequence represents a B. napus Sac66 protein putative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Fig 15; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wyatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                         KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG
                                                                                                                                                                                                 QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                 NNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNBACSSRTPVQFVVPKNKNYLL
        QNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMFNCSVKYPCQGIVLENVNIKG-
                                  QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
                                                                SLGDDNSKAYVSGINVDGATLSETDNGV
                                                                                                                                                                           KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK
                                                                                                                                                                                                                                                                                                                                             AIFLCVLLMLACCQALSSNVDDGYGHEDGSFET--DSLIKLNNDDDVLTLKSSDRPTTES
                                                                                          SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                       ITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGISIG
                                                                                                                                                INASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIG
                                                                                                                                                                                                                                   KSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDKNHWLILEDVNNLSIDGGSAGIVDGNG
                                                                                                                                                                                                                                                                                                                                                                         SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; dehiscence; maie su
oilseed rape; Sac66 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     46.2%;
                                                                                                                                                                                                                                                                                         --TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLIPKGKTYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 1103; DB
Pred. No. 1e-84;
70; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehiscence; male sterile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative sequence
                                                                                                                                                                                                                                                                                                                                                                                                      125;
                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Length 433; Indels

present

or

28;

Gaps

99 61

protein;

355

IKFQNIRMDNVKNPIIID

354

358

298 234 238

294

178 114 121

174

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ARESULT 15
AAR48674
ID AAR486
XX AAR486
AC AAR
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                                                                                                                                                                                                                                                                                                                                                                              During early ripening of peaches, tissue firmness decreases slowly and compressively. Towards the end of ripening, loss of tissue firmness is capid. This second stage of softening is called the "melting" stage. Compide the peach varieties used for caming do not have a "melting" phase confusion. Ripe fruit remain relatively firm and maintain their shape throughout processing. Fruit of "melting" varieties show an increase in cathvity of endopolygalacturonase (Endopa) during ripening. Complete through its action on intercellular and cell wall pectins. The sequence can be used to manipulate plants of the Rosaceae family, especially peach or prunus to either prevent or enhance capression of PG. The sequence can also be used in efficient breeding programmes. See also ARA48675, ARA48676. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                    Query Match
Best Local S
Matches 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ripening; melting; pectins; breeding; Prunus; Rosaceae; endopolygalacturonase; EndoPG; polygalacturonase; PG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003
25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding peach polygalacturonase (PG) and production of peach PG in rosaceae plants - for production of plants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-101199/12.
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 37-38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-melting' phenotype.
                                                                                                                                                                                                                    Local Similarity
mes 210; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMONWEALTH SCI & IND RES ORG PACIFIC SEEDS PTY LTD.
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                                                                                                                                              NGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPC
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                                                    RSSISVKIFGSLEASSKISDYKDRRIWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINK 190
                                                                                                           SSVKTISIANFGAKGNGAD-DTRAFEKAWKAACSSNGAIVLVVPQ-KTYLVRPIEFSGPC
                                                                                                                                                                                                                                                                                                                                  404 AA;
  KSHLTMTIYGTIBASDDRSVYKDVTHWLIFDNVQSLLVVGPGWINGNGNRWWETHAK--E
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                    44.2%;
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                                                                                                                                                                                                                      Score 1056.5;
Pred. No. 8.2e
50; Mismatches
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1.2e-81;
les 94;
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 NVKPAYKGAVSPRCS
                             NVHFNNAEHVTPHCT 443
                                                            TRORSAVOVKNVLYONIRGISASTDAITENCSOSVECOGIVLONIOL---
                                                                                                                          SGVFVNGAKISGTSNGVRIKTWQGGSGSASNIVFQNVEMNDVTNPIIIDQNYCDHKNKDC
                                                                                                                                                   SNYTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCD-RVEPC 368
                                                                                                                                                                                        GIHITNTKNITISSSVIGTGDDCISIVSGSQRVQATDITCGPGHGIRIGSLGEDNANDHV
                                                                                                                                                                                                          GVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSIGSGSGNSEAYV 309
                                                                                                                                                                                                                                                      SLRPCTNTPTAVTPNKCNNLVVKNLKIQYAQQMHVRPQNCKNVEASHLTVTAPEDSPNTD
                                                                                                                                                                                                                                                                   SL-PCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTD
 399
                                                               -- QNARAKCN
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Search completed: July 21, 2004, 17:06:20 Job time : 99.9229 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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N_Geneseq_29Jan04:*
1: geneseqn1980s:*
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                                                                                                                                                                                                                                                                                                                                                                  IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	14.8	15.2	15.2	18.1	18.9	20.2	20.3	20.3	20.3	20.3	22.6	22.9	23.9	25.6	25.7	25.7	27.2	27.2	63.7	98.5	99.3	00.	100.0	Match		o <del>/</del> P
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WPI; 1993-087084/11. P-PSDB; AAR32107. Recombinant DNA for flower control - comprises base s sequence of bases compleme encoding softening enzymes Example 12; Fig 1; 20pp; E.	17-MAK-1993.  06-NOV-1987; 92EP-00117411.  11-NOV-1986; 86GB-00026879.  (ICIL ) IMPERIAL CHEM IND PLC. (ZENE ) ZENECA LTD.  Bridges IG, Grierson D, Schuch	DE Polygalacturonase cDNA clone pTOM6.  XX  XW polygalacturonase; PG; pectin esterase; PE; expression regulation;  XW polygalacturonase; PG; pectin esterase; PE; expression regulation;  XW fruit softening enzymes; flowering plants; fruiting plants;  XX  XX  CS Lycopersicon esculentum.  XX  Y-COS  Y-COS	ALIGNMENTS  RESULT 1  AAQ38415  ID AAQ38415 standard; DNA; 1636 BP.  XX  AC AAQ38415;  XX  DT 27-AUG-2003 (revised) DT 25-MAR-2003 (revised) DT 05-JUL-1993 (first entry)  XX	24         236.6         14.5         1505         3         AAC50895         AAC50895         Arabidops           25         228         13.9         1470         2         AAQ66049         Aaq66049         Japanese           26         228         13.9         1479         2         AAQ66051         Appanese           27         228         13.9         1726         2         AAQ66050         Aaq66048         Japanese           28         225.4         13.8         1395         2         AAQ66050         Aaq66050         Japanese           30         224.8         13.7         1542         2         AAQ66050         Aaq69050         Aaq6000         Aaq66050         Japanese           31         224.8         13.7         1733         2         AAT18102         Aaq84046         Japonicum           32         224.8         13.7         1733         2         AAT18102         Aaq84046         Japonicum           32         224.8         13.7         1733         2         AAT18102         Aaq84044         Japonicum           32         21.1         13.5         1380         23.4         AAQ84044         Aaq84044         Japonicum

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XX EFH KEY Pectin; pectin methylesterase; PME; polygalacturonase; PG; tomato; food product; yogurt; milk; fruit juice; whey drink; de-esterification; cDNA sequence 20-APR-2001 AAC84653 Lycopersicon ss. standard; esculentum (first entry) of f Location/Qualifiers 51. .1424 pTOM6 encoding a polygalacturonase CDNA; 1636 ВP

(PG)

enzyme

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The invention provides a new method for modifying pectin that involves CC providing a host having pectin methylesterase (PME) activity and CC polygalacturonase (PG) activity, transforming the host by silencing PG CC activity to provide an increased PME to PG ratio, preparing a PME extract CC PME modified pectin is useful for foodstuffs preparation, and to impart CC an increased functionality to food products such as yogurt, milk/fruit CC juice and whey drinks. PME is useful to reduce the number of ester groups CC in a pectin in a block-wise manner, and to de-esterify two or more CC adjacent galacturonic acid residue of a pectin on at least substantially CC sequence of pTOM6 encoding a PG enzyme. A nucleotide sequence (seq Id No. 3) encoding the PG enzyme which is deposited as pTOM23 with NCIMB CC is not provided in the senerification.
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Matches 1636
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                                                                                Query Match
Best Local Similarity
Matches 1636; Conserv
                                                                                                                                                  This cDNA clone, encoding polygalacturonase (PG), is used to produce antisense mRNA (with an inverted sequence to that of PG mRNA) which is inserted into a vector used to transform plants which thereafter have altered ripening properties. The inverted sequence and the PG mRNA form double-stranded structure which inhibits expression of the PG mRNA. See also AAN80488. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                       (ICIL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid clone
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20-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1986;
                                                                                                                                                                                                                                                         Recombinant DNA comprising promoter and terminator sequences plants for altering ripening properties esp. in tomatoes.
                                                                                                                                                                                                                                                                                                         WPI; 1988-169271/25
                                                                                                                                                                                                                                                                                                                              Bridges IG,
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51. .1424
/*tag= a
/label= polygalacturonase
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                                                   TGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAA
                              TGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAA
                                                                                                                     AAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATACTATTAT
                                                                                                                                                                     TGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCC
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                                                                                                                                                                                                                                                            CAPAPATTTGAAAGTGAATAATCTAAAGAGTGAAAAATGCACAACTAATTCATATCAAATT
                                                                                                     AAATACTGATGGAGTCCATGTATCAAATACTCAATATATTCAAATATCTGATACTATTAT
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Pred. No. 4.6e-273;
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The present invention relates to an improved method for inhibiting the CC expression of a target gene in a cell, by expressing in the cell an CC expression cassette comprising a promoter operably linked to a sense or CC entitled in the cell an inverted repeat (IR) of a subsequence of the targeting sequence having substantial identity to a subsequence CC of the target gene, and an inverted repeat (IR) of a subsequence of a NOS CC (nopaline synthase) gene, where the IR is unrelated to the targeting CC (sequence. The expression cassette, pPF-IRN1 is constructed using a CC (s-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato CC (s-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato CC (polygalacturonase (PO) gene and an IR of the terminator of the CC polygalacturonase (PO) gene and an IR of the terminator of the Expression of endogenous genes and transgenes, e.g. to regulating expression of endogenous genes and transgences, e.g. to regulate CC expression of endogenous plant phenotypes such as disease resistance, if lavour, protein or nutritional characteristics. The improved gene CC effect of regulating gene expression of a selected endogenous gene or transgene. The method is simple and rapid, and is suitable for hightoning the construct can be silenced at the same time, since the initial silencing trigger mediated through the inverted repeat region will apply to castlet a protein and transcripts. The present sequence represents the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reducing the expression of a target gene in a cell, comprises expressing in the cell an expression cassette comprising a promoter operably linked to a sense or antisense targeting sequence and an inverted repeat of a
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07-AUG-2001;
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Matches 1046; Query Match Best Local 1439 376 436 Similarity CAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTTAGTTGTTG CATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGAAGCATCTAGTAAAATTT TTANANCCATGGTTCCTANANCANGANTTATCTTCTCANGCANATCACCTTTTCAGGTC 1438 TTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTC CATGCAGATCTTCTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTT Conservative 63.7%; 99.4%; 0; Mismatches Score 1042.4; DB 6; Pred. No. 2.1e-173; 6; Indels Length 5822; 0;

Sequence 5822 BP; 1689 A; 1275 C; 1292 G;

1566 T; 0 U; 0 Other;

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ATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATT GAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCAAAATAA GAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCAAAATAA 615 CAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTAGTTGTTG

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pathogenic infecti bacterial, fungal g at least infection fungal or one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant to

Claim 6; SEQ ID NO 557; 899pp; English

comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression is significantly altered in expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present semicone.

Sequence 1296 BP; 424 A; 244 C; 293 G; 335 н, 0 ٦, 0 Other;

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Match

Similarity

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Length 1296;

В 8 Дò Ś 밁 5 멍 Š B δ 뮍 Š 뮍 8 δÃ 뮍 Ъ Ş δÃ 밁 B S Matches Local 720; 803 871 683 751 623 563 691 631 503 443 383 457 GTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTG CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG CAAATACTCAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTT CCATTGAGGATGGAAAGCTAAAATCTTCAAATCTTTGATTTAACTTGCGGCCCCGGTCACG CTAATACTCAAAACATTCGAGTCTCCAACTCAGATATCGGAACAGGTGATGATTGTATAT TTAGTAATGTTGAGATCACTGCTCCGGGCGATAGTCCCAACACAGATGGTATCCATATCA CTTCAAATTTGATGATGAATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTAT TGAGGGTGAAAAATGCGCAGCAGATTCAGATTTCAATTGAGAAATGCAACAAAGTTGAAG TAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAG GCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAATTTGAAAGTGAATAATC GCACAAAAGCTCCAACGGCTCTTACTTTATACAATTTAAAGAATTTGAATGTGAAGAATC TTAATGGCAACGGAAAAACCTGGTGGCAGAACTCATGCAAAATCGACAAATCTAAGCCAT TTTGGATTGCTTTTGATAGTGTTCAAAATTTAGTTGTTGGAGGAGGA-----TTCAGATCCTAGGCACTTTATCAGCATCTACGAAACGTTCAGATTACAAAGACAAAAACC TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTACAAAGATAGAAGGC GAAAGACTTATCTCCTTAAGTCTACTCGATTTAGAGGCCCATGCAAATCCTTACGTAACT ACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAA 396 AGAAAGCATGGAAGAAAGCATGTTCAACAAATGGAGTTACTACTTTCTTGGTTCCTAAAG TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAACATATGATAATATTGCATTTG TTAGTGTTTCAAACTTCGGAGCCAAAGGAGATGGAAAAACTGATGATACTCAGGCCTTCA Conservative 'ATCTTAGAGGACGTTAACAATCTATCAATCGACGGTGGCTCGACGGGAATTA 0; Score 445.2; DB 7 Pred. No. 6.5e-69; 0; Mismatches 368 368; Indels 24; -GGAACTA 862 802 870 810 502 742 682 750 622 690 562 630 570 442 382 456 336 516 322 262

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                   TGGATGGTGCTAAGTTCTCTGAGAGTGACAATGGAGTTAGGATTAAGACTTATCAGGGAG
                                      TAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAG
                                                                            GTATAAGTATTGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTTGTCTAATGTTACTG
                                                                                                                      CAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATG
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A cDNA clone (AAT33994), designated SAC66, codes for a polygalacturonase (AAW04248) that is expressed specifically in the dehiscence zone (DZ) of oilseed rape cv. Rafal seed pods. Degenerate PCR primers based on multiple sequence alignments of fruit- and pollen-specific polygalacturonases were used to amplify cDNA from the DZ. A PCR fragment (AAT33999) was generated and used to screen a DZ CDNA library, yielding clone SAC66. The gene can be used in transgenic crop plants to regulate pod dehiscence. Antisense sequences reduce or prevent dehiscence and hence loss of seed prior to harvesting. (Updated on 16-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2003
14-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT33994;
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                                                                                                                                                                                                                                                                                                                                                                                                 Oilseed rape
                                                                                                                                                                                                                                                                                      WO9630529-A1
                                                                                                                                                                                                                                                                                                                                               Brassica napus; cv. Rafal.
                                                                                                                                                                                                                                                                                                                                                                    transgenic
                                                                                                      Claim 6;
                                                                                                                      Control of seed pod dehiscence - using polygalacturonase sequences derived from polygalacturonase gene.
                                                                                                                                                                WPI; 1996-455374/45
                                                                                                                                                                                  Roberts JA,
                                                                                                                                                                                                                          31-MAR-1995;
                                                                                                                                                                                                                                             29-MAR-1996;
                                                                                                                                                                                                                                                                 03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                              Polygalacturonase; seed pod;
                                                                                                                                                                                                       (NICK-) NICKERSON BIOCHEM LTD
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                                                                                                    Fig 1; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCTGAACATGTTACACCACACTGCACTTCA
                                                                                                                                                                                                                                                                                                                                                                   plant; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                 seed
                                                                                                                                                                                   Coupe
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(first entry)
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                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                pod polygalacturonase
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                                                                                                                                                                                    Jenkins
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                                                                                                                                                                                                                                                                                                                                                                               dehiscence; shatter; oilseed rape;
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                                                              CAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGG
                                                                                                              ATCCGATCATAATCGACCAGAACTACTGCGA---CAAGGACAAATGCGAACAACAAGAAT
                                                                                                                                                ATCCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTT
                                                                                                                                                                                    GAGGGTCAGGAACTGCTAAGAACATTAAATTCCAAAACATTCGTATGGATAATGTCAAGA
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TGGCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATA
                                      CTGCGGTTCAAGTGAACAATGTCGTGTATCGGAACATACAAGGTACGAGCGCAACGGATG
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Pred. No. 1.5e-64;
0; Mismatches 416;
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Transgenic plant containing dehiscence zone selective chimeric
                    WPI; 1997-235901/21
                                          Ulvskov P,
                                                                            08-DEC-1995;
                                                                                     06-0CT-1995;
                                                                                                     04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2003
25-MAR-2003
08-JUL-1997
                                                             (PLBZ ) PLANT
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                                    Child R,
Petersen I
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cDNA clone X (AAT63603) includes a coding sequence for oilseed rape dehiscence zone (DZ)-selective endopolygalacturonase (PG). DZ cDNA was subjected to PCR amplification using primers (see also AAT63605-08) based on conserved regions of PG amino acid sequences. PG-related clones (see also AAT63609-14) were identified, of which only Ipg35-8 was specific to the DZ. This clone was used to screen a DZ-selective cDNA library prepd. K. Ipg35-8 was also used from the DZ 6 wk after anthesis, yielding clone x. Ipg35-8 was also used to screen a genomic library to identify the DZ-britised in novel chimeric genes to modify the dehiscence properties of transgenic plants, partic. the pod dehiscence properties of E. napus. 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                   modified dehiscence properties, especially delayed pod dehiscence
                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                           65pp; English.
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Š Best Loc Matches Query Match Sequence 1631 BP; 554 A; 291 C; 339 G; 446 T; Local 717; Similarity Conservative 25.7**%;** 63.6**%**; 0; Score 420.2; DB 2 Pred. No. 1.6e-64; 0; Mismatches 383 383; 0 U; 2; Length 1631; Indels 1 Other; 27;

840 808 889 720 600 568 4.80 457 420 397 ACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG 360 300 ATGGGATCAGCATTGGAAGCTTGGGGGGATGACAATTCCAAAGCTTATGTATCGGGAATTG AIGGTATAAGTATIGGAAGCTTAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTA 987 TCGTTGCTACTAAAAACATTCGAATCTCCAATTCAGACATTGGGACAGGTGATGATTGTA TATCAAATACTCAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTA GCGTTAAGAATGTTAAGATCACTGCTCCTGGCGATAGTCCCCAACACGGATGGTATTCATA TAGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATG ATCTAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTG CATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATA TTGTTGATGGCAACGGAAATATCTGGTGGCAAAACTCATGCAAAATCGACAAATCTAAGC TITCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTC ATCTGAGAGTGAGAATGCACAGCAGATTCAGATTTCGATTGAGAAATGCAACAATGTTG CATGCACAAAAGCGCCAACGGCTCTTACTCTCTACAACCTAAAGAATTTGAATGTGAAGA ACCACTGGCTTATTTTGGAAGACGTTAATAATCTATCAATCGATGGCGGCTCGGCGGGA GGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTA-----TCCAGATCCTAGGCACTTTATCAGCTTCTACAAAACGATCGGATTACAGTAATGACAAGA TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTAC---AAAGATAGAA GAAAGACTTATCTCCTTAAGTCTATTAGATTCAGAGGCCCATGCAAATCTTTACGTAGCT 479 AGAAAGCATGGAAGAAGGCATGTTCAACAAATGGAGTTACTACTTTCTTAATTCCTAAAG 419 AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTTGTGGTTCCTAAAA 396 TTAGTGTTTCGAACTTCGGAGCCAAAGGAGATGGAAAAACCGATGATACTCAGGCTTTCA 359 TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAACATATGATAATATTGCATTTG 336 GTTGTTGGAGGAGGAG 959 927 899 839 747 627 867 807 779 719 687 659 567 539 513 599

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                                  The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The press sequence represents the DNA encoding a B. napus Sac66 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal transduction protein; dehiscence; male sterile plant; shatter resistance; oilseed rape; Sac66 protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                  Sequence
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Katagiri
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  TGAATGCGTGGAAGAAAGCATGTTCTTCAAATGGAGCTGTTAATCTCCTAGTTCCTAAAG
                                                                                                           TTAGTGTTTCTGATTTTGGAĞCTAAAGGAĞATĞĞAAAAACCGATĞACACGCAĞĞCGTTCG
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F, Quan
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Katagiri
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               Producing transgenic plant of modified phenotype - is usefuexpression of heterologous genes which are light-inducible
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88US-00188361.
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93US-00105852.
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87US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue-specific gene expression;
pression; polygalacturonase; toma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic
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                                   is useful
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Best Local Similarity
Matches 342; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a tomato polygalacturonase genomic DNA clone isolated from a genomic library by screening with polygalacturonase cDNA. The polygalacturonase gene promoter is active in at least the breaker through red fruit stage in tomato fruit, and can be used in a novel method of the invention for producing a plant with an altered phenotype. In this method, regulatory regions from genes expressed during a particular developmental stage or in a specific tissue are identified by cDNA screening. The regulatory regions are manipulated for use with foreign sequences for introduction into plant cells to provide transformed plants having a phenotypic property that can be modulated. The invention is exemplified with light, seed and fruit-specific promoters. Transformation without gall formation of cells which are not Agrobacterium hosts, especially cereals and legumes, is achieved. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2207 BP; 870 A; 282 C; 270 G; 784 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 174; Fig
 17-JAN-1985;
31-JUL-1986;
26-MAY-1987;
                                                                                                                                                                                          Transgenic plant; tissue-specific gene expression; fruit-specific expression; tomato; polygalacturonas
                                                                                                                                                                                                                                                                        25-MAR-2003
26-OCT-1998
                                                                                                                               US5753475-A
                                                                                                                                                              Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                        AAV36973;
                                                                                                                                                                                                                                                                                                                                                      AAV36973 standard; DNA;
                                                                  10-AUG-1993;
                                                                                               19-MAY-1998
                                                                                                                                                                                                                                         Polygalacturonase genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAATGTTATTGATGACAATTTATTCAAACAAGTTTATGATAATATTCTTGAACAAGAAT 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGGAATAGTATTCTCCTTCTCATTATTATTTTTGCTTCATCAATTTCAACTTGTAGAA 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTGGAGCTA
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(first en
   85US-00692605.
86US-00891529.
87US-00054369.
                                                                                                                                                                                            expression; tomato; polygalacturonase;
                                                                  93US-00105852
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Pred. No. 4.7e-49;
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This is the nucleotide sequence of a tomato polygalacturonase genomic DNA Clone isolated from a genomic library by screening with polygalacturonase CDNA. The polygalacturonase gene promoter is active in at least the CC breaker through red fruit stage in tomato fruit, and can be used in a CC breaker through red fruit stage in tomato fruit, and can be used in a CC phenotype. In this method, regulatory regions from plant genes (and T-DNA CC and Ti or Ri plasmids) are manipulated for use with foreign sequences for introduction into plant cells to provide transformed plants having a CC phenotypic property that can be modulated. The invention is exemplified CC with light, seed and fruit specific promoters. Also claimed are methods CC with light, seed and fruit specific promoters. Also claimed are methods CC tissue, modifying the genotype of a plant to impart a desired characteristic to fruit, modifying transcription in fruit tissue, and CC expressing a heterologous DNA sequence of interest specifically in fruit CC tissue. The method provides transformation without gall formation in CC plants which have historically not been Agrobacterium hosts. (Updated on CC 25-MAR-2003 to correct PR field.)
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Best Local Similarity
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25-JAN-1988;
15-MAR-1988;
29-APR-1988;
02-NOV-1988;
02-NOV-1988;
21-MAY-1990;
09-JUL-1990;
14-SEP-1990;
08-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Fig 8A-C; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transformation of plants - with regulatory for tissue specific expression of genes.
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                                                                                                                                   TTGCTCATGATTTTCAAGCTTATCTTTATTTGAGCAAAAATATTGAAAGCAACAATA
                                                                                                                                                                                                    GCAATGTTATTGATGACAATTTATTCAAACAAGTTTATGATAATATTCTTGAACAAGAAT
                                                                                                                                                                                                                         GCAATGTTATTGATGACAATTTATTCAAACAAGTTTATGATAATATTCTTGAACAAGAAT 180
                                                                                                                                                                                                                                                                                                                                      AATCTTTTTCAATAGACAAGTTTAAAAACCATACCATATAACAATATATCATGGTTATCC
                                                                                                                                                                                                                                                                                                                                                             AATCTTTTCAATAGACAAGTTTAAAAAACCATACCATATAACAATATATCATGGTTATCC
                                 ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGATTAATGTACTTAGCTTTGGAGCTA 300
                                                                                                                                                                 TTGCTCATGATTTTCAAGCTTATCTTTCTTATTTGAGCAAAAATATTGAAAGCAACAATA
                                                                                                                                                                                                                                                                       <u>AAAGGAATAGTATTCTCCTTCTCATTATTATTTTTGCTTCATCAATTTCAACTTGTAGAA</u>
AGGGTGATGGAAAAACATATGATAATATTGTAAGTATTTAAATATTGGAATATATTTGT
                                                                    ATATTGACAAGGTTGATAAAAATGGGATTAAAGTGA
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88US-00147781.
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Search completed: July 26, Job time : 674 secs

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APPLICATION NUMBER: 419,779
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APPLICATION NUMBER: 119,614
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Matches
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APPLICANT: COUPE, Simon Allan
APPLICANT: COUPE, Simon Allan
APPLICANT: JENKINS, Elizabeth Sarah
APPLICANT: JENKINS, ENZAbeth SARAH
TITLE OF INVENTION: CONTROL OF POD DEHISCENCE
                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/941,532
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00757
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9506684.1
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                               TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                          NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGERENCE, DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                     FEATURE:
NAME/KEY:
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TELEPHONE: (202)
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                 TTAATGTACTTAGCTTTGGAGCTAAGGGTGATGGAAAAACATATGATAATATTGCATTTG
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                                                              Conservative
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                                                              Score 420.4; DB 3;
Pred. No. 2.8e-87;
0; Mismatches 416;
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                                                  ACAATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTTCAGAGGATGAAGCTC
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SOFTWARE: Pace
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FRIGHT: 1631
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APPLICANT: BUNDGARD
APPLICANT: BOTTERMAN
TITLE OF INVENTION:
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OTHER INFORMATION: 0
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PRIOR APPLICATION NUMBER: EP 95
PRIOR FILING DATE: 1995-12-08
NUMBER OF SEQ ID NOS: 14
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CURRENT APPLICATION NUMBER: US/09/051,239A
CURRENT FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: PCT/ED96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR FILING DATE: 1995-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
ILOCATION: (95)..(1393)
OTHER INFORMATION: Location 821-837 = region of endo-PG
OTHER INFORMATION: corresponding to oligonucleotide PG1.
OTHER INFORMATION: Strain cv. Topaz.
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OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                           Local Similarity
mes 717; Conserv
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                          TAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTTCAGACTAC----AAAGATAGAA
                                                                                                                                                                                                               TTAGTGTTTCGAACTTCGGAGCCAAAGGAGGAGATGGAAAAACCGATGATACTCAGGCTTTCA
                                                                     GAAAGACTTATCTCCTTAAGTCTATTAGATTCAGAGGCCCATGCAAATCTTTACGTAGCT
                                                                                                    ACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAG
                                                                                                                                                                           AGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAA 396
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TCCAGATCCTAGGCACTTTATCAGCTTCTACAAAACGATCGGATTACAGTAATGACAAGA
                                                                                                                                           AGAAAGCATGGAAGAAGGCATGTTCAACAAATGGAGTTACTTCTTTAATTCCTAAAG
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BOTTERMAN, JOHN
BOTTERMAN, JOHN
BOTTON: Seed S
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BUNDGARD POULSEN,
BOTTERMAN, Johan
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BORKHARDT, Bernard
SANDER, Lilli
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VAN ONCKELIN, Henri
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location 95-163 = region encoding the presumed endo-PG signal peptide.

Location 884-900 = region of the endo-PG cDNA corresponding to oligonucleotide PG3

Location 1059-1073 = region of the endo-PG cDNA complementary to oligonucleotide PG2

Location 1229-1245 = region of the endo-PG cDNA complementary to oligonucleotide PG2
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Pred. No. 3.1e-87;
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                                                    Sequence 139, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT:
APPLICANT:
APPLICANT:
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Kuo, Mei-Chang;
Yeung, Siu-mei H.;
                                      Garman,
                                        Richard D;
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/350,22:
APPLICATION UNMBER: 08/350,22:
APPLICATION UNMBER: 08/350,22:
APPLICATION UNMBER: 0.25:
APPLICATION NUMBER: 38,872
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 025:
REFERENCE/DOCKET NUMBER: 025:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-740
TELEPAX: (617) 227-740
TELEPAX: (617) 227-7941
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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TOPOLOGY: li
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                            GGCCAATGTAAATGGGTCAATGGACGAGAAATTTGCAACGATCGTGATAGACCAACAGCC
                                                                  AGTTCTTGCAAAATAAATAAATCACTGCCA-----TGCAGGGATGCACCAACGGCC
                                                                                                        ACAGGTTTTACTCTAATGGGTAAAGGTGTAATTGATGGGGCAAGGAAAACAATGGTGGGCT
                                                                                                                                            CAAAATTTAGTTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCA 599
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pred. No. 3.4e-43;
0; Mismatches 495; Indels 1
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RESULT 5
US-08-467-023-141
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Patent No. 6090386
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                   APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Prot
TITLE OF INVENTION: Japanese Cedar
NUMBER OF SEQUENCES: 261
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical
                                                                         COUNTRY: U
ZIP: 02154
                                                                                                                                          STREET:
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Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                                                         Kuo, Mei-Chang;
Yeung, Siu-mei H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 0.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Jane E. Remillard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 13.9%; Local Similarity 52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: Decemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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EDNESS: single
AATGTGCAGGCCACAAATATTACTTGTGGTCCAGGTCATGGTATAAGTATTGGAAGCTTA
                                         TTACAAAAGAACACGATAGGAACAGGGGATGACTGCGTCGCTATAGGCACAGGGTCTTCT
                                                                                          ATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAA 890
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Pred. No. 3.4e-43;
0; Mismatches 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMI-028CPD2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
                                                         REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                 FILING DATE: December 6, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                          NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U. ZIP: 02154
                                                                                                                                                                                         APPLICATION NUMBER: 08/350,225
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Exley, Mark A.;
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Yeung, Siu-mei H.;
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Bond, Julian F.;
Garman, Richard D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrew;
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Best Local Similarity
Matches 557; Conserv
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LOCATION:
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           <u>ATAATTTATGAGAATGTTGAAATGATAAATTCGGAGAACCCCATATTAATAAATCAATTC</u>
                                                                                    GACACACAAAATGGATTAAGAATCAAAACATGGCAGGGTGGTTCAGGCATGGCAAGCCAT
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Pred. No. 3.6e-43;
0; Mismatches 495;
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Matches
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY_AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 025.6
REFERENCE/DOCKET NUMBER: 025.6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Allergenic Proteins And
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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COUNTRY:
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CITY: W
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08 FILING DATE: June 6, 1995 CLASSIFICATION: 424
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TELEFAX: (617) 227-5941
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   TCATGATGCTATCAACATCTTCAATGTGGAAAAAGTATGGCGCAGTAGGCGATGGAAAGCA
                               GACAGTATGCCCTGCAAAGATATAAAGCTAAGTGATATATCTTT
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Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuo, Mei-Chang;
Yeung, Siu-mei H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garman,
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Bond, Julian F.;
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                                                                                  13.8%;
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                                                              Score 225.4; DB 3;
Pred. No. 1.3e-42;
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US-08-463-213-1
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                                                                           AGATATAAAGCTAAGTGATATATCTTT
                                                                                                         AGGAATTATAATGGAGAATATAAATTT 1294
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Best Local Similarity
Matches 212; Conserva
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APPLICATION NUMBER: 06/920,574
FILLING DATE: 17-OCT-86
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/845,676
APPLICATION NUMBER: 06/845,676
ATTORNEY/AGENT INFORMATION:
NAME: 11/25beth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
NAME: Donna E. Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (916) 753-15
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NIMBER: 07/750,505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTI-SENSE REGULATION OF GENE TITLE OF INVENTION: EXPRESSION IN PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 27-AUG
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CITY: Davis
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FILING DATE: 30-AUG-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
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                                                                    ATAATATTGCATTTGAGCAAGCATGGAATGAAGCATGTTCATCTAGAACACCTGTTCAAT
TTGTGGTTCCTAAAAACAACAATTATCTTCTCAAGCAAATCACCTTTTCAGGTCCATGCA
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                (916)
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IN PLANT/CELLS

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07

FILING DATE: 27-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 240,40

FILING DATE: 30-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
5453566-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-941-532-7
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 212; Conserva
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   APPLICANT: ROBERTS, Jeremy Alan
APPLICANT: COUDE, Simon Allan
APPLICANT: JENKINS, Blizabeth Sarah
TITLE OF INVENTION: CONTROL OF POD DEHISCENCE
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 219
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FILING DATE: 17-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-MAR-1986
                                                                                                                                                                                                               STREET:
APPLICATION NUMBER: US/0 FILING DATE: 30-SEP-1997
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                             17, APE NO. 6096946
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                US/08/941,532
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RESULT 11
US-08-232-463-14/c
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB
FILING DATE: 29-WAR-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 950
PILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                      STREET: 1000
                                                         FILING DATE:
CLASSIFICATION: 435
 APPLICATION NUMBER:
                FILING DATE:
                                                                                                                                                                                                     COUNTRY:
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                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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1800 Diagonal Road, Suite
                                                                                                                                                                                                       USA
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EP 91 114 300.6
                            US/07/935,313
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Pred. No. 5.6e-08;
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                                                                                                                 #1
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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1092 RRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCT 1053
                              1290 AATTTAGTAGGGGAAAAGTGGAAAACCATCAGAGGCTACGT 1329
                                                                                                                                              1170 GCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGCAACAAAGGTG 1229
                                                                                                                                                                                  1272
                                                                                                                                                                                                       1110 CCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCA 1169
                                                                                                                                                                                                                                                                                             1230 GCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAATGGAGAATATA
                                                                                                                    990 GTAAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGA 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 5.0%;
                                                          nucleic acid
                                                                                                                                                                             GGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTAT 1109
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RESULT 12
US-09-790-988-1
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; Patent No. 6632935
; Patent No. 16632935
; Patent No. 1672935
; APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SAKAH, YOSHIYUKI
ITITLE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APPLICANT
CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: UP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; SEQ ID NO 1
; SEQ ID NO 1
; PRIOR HILLIGED DATE SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; PRIOR HILLIGED DATE SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; PRIOR HILLIGED DATE SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1

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Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125;
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                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2998: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451 GCAGATATGATATCACAATAAACAAATCTATATCTATGTATTGAATAATTATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1391 TTCAGAGGATGAAGCTCTTTTGTATAATTATTATTATATTATACTATAGATCTTCAATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1631 AAAAA 1635
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
              HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
ORIGINAL SOURCE:
                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAA 325389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAAATATTTTATATTTTAATAAAAATACATTTTATATAAATAAATACTGATATTTT
                                                                                               STRANDEDNESS:
                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                               TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                       LENGTH: 1356 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                               double
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Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 640681;
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; NAME/KBY: misc feature; LOCATION: (B) LOCATION 1...1356; SEQUENCE DESCRIPTION: SEQ ID NO: 2998: US-09-107-532A-2998
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                                                                                                                                                                                                                                                                                                              APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DIA OF BACTERIAL SYI
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: UP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-790-988-1/c
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GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                          LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera
                                                                                                                                    hes 154;
                                                           609613 AAAGTAGCAATTTCAATAATACGATGTACTTTAGGATTCAGTCCAGTCATTTCTAAATCT
                                                                                          1333 AAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTTCACTAGAAATTT
1393 CAGAGGATGAAGCTCTTTTGTATAATTATTATTTATACTATAGATCTTCAATATATAGC 1452
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                                                                                                                                                                                                                                                              640681
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                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCAGTCACCAAGTTGGACGATCAACCCGATTCTTTGCAGTAATGCAACGTTTGATAAC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GÇACCAACGGCCTŢAACCŢŢĊŢGGAAŢŢĠCAAAAŢŢŢĠAAAGŢĠAAŢAĀŢĊŢAAAGAGŢ 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGGATCTCAAAATGTGCAGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAATGCACAACTTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAAT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTABATTG---ATGAGTTTCCATAACTGTCATCGAATTACTGTGAAAGATATTAAATTG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGGACTGAAGATACGTACG 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAAATGTGCGTATTAGTAATTGCCATATTGACGTGGGAGATGACTGTATTGCAATCAAG 639
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                                                                                                                                  Conservative
                                                                                                                                                   3.2%;
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47.9%; Pred. No. 0.0061;
tive 0; Mismatches 19
                                                                                                                                  Score 52; DB 4; Length 640681;
Pred. No. 0.059;
0; Mismatches 145; Indels 5
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QY 1610 GTTATTTATATGAAAAAAAAAA 1632	QY 1550 TCTATTTTCTAGTCAAAAGITTGACGATTGTACTTTTTAATGTACAAAAATAATAAAAGG	OY 1490 GTATTGAATAATTATTATTAATATGTACGGATTGAAGTTTTAATAAGACTACTATGTATT	2346	Db 2406 ACACTACTCTAAACTCTAAAAACTTACTAATAAAAAACGAAACATAAA	Qy 1370 ACACTGCACTTCACTAGAAATTTCAGAGGATGAAGCTCTTTTGTATAATTAAT	Query Match 3.2%; Score 51.8; DB 4; Length 6: Best Local Similarity 49.8%; Pred. No. 0.014; Matches 131; Conservative 0; Mismatches 132; Indels	OTHER INFORMATION: chemically treated genomic DNA (Homo s'S-10-204-708-19	. w.	SEQ ID NO 19 ; LENGTH: 6866	PRIOR FILING DATE: 200	PRIOR APPLICATION NUMBER: DE 10032529. PRIOR FILING DATE: 2000-06-30	PRIOR APPLICATION N	PRIOR APPLICATION N	PPLICATION NUMBER: PCT/	CURRENT APPLICAT	TITLE OF INVENTION: by Assessing DNA Methylation FILE REFERENCE: 5013.1012	TITLE OF INVENTION: Diagnosis of Diseases Associated with	POT TORREST PROPERTY OF THE PR	APPLICANT: OIEK, Alexander	Patent No. 6677731 GENERAL INFORMATION: APPLICANT: OLEK, Alexander APPLICANT: DIENBROOF Ch	S-10-204-708-19/c Sequence 19, Application US/102047 Pateent No. 6677731 GENERAL INFORMATION: APPLICANT: DIEENBOOGE APPLICANT: DIEENBOOGE APPLICANT: DIEENBOOGE	SULT 15 -10-204-708-19/c Sequence 19, Application US/ Patent No. 6677731 GENERAL INFORMATION: GENERAL OLEK, Alexander APPLICANT: OLEK, Alexander	SULT 15 -10-204-708-19/c Sequence 19, Application US/ Patent No. 6677731 GENERAL INFORMATION: APPLICANT: OLEK, ALEXANDER APPLICANT: DIESPENDEDCO	SULT 15 -10-204-708-19/C SEQUENCE 19, Application US/ PATENT NO. 667731 GENERAL INFORMATION: APPLICANT: DIEK, Alexander APPLICANT: DIEK, Alexander APPLICANT: DIEK, Alexander	609378 TTGATTAGATATATAT  1633 AAAA 1636            609318 AATA 609315  SULT 15 -10-204-708-19/c -10-204-708-19/c SEQUENCE 19, Application US PALENT NO. 6677731 GENERAL INFORMATION: APPLICANT: DIEBENDEON COLEK, Alexander APPLICANT: DIEBENDEON COLEK	1573 ACGATTGTACTTTTAA	1573 1573 609378 609378 1633 1633 1633 1736 1737 170-204-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-1 170-204-708-708-708-1 170-204-708-708-708-708-708-708-708-708-708-708	1513 TGTACGGATTGAAGTTT	1513 1513 1609438 1609438 1673 1674	1453 1609493 1513 1609438 1609438 1573 1609378 1609378 1633 1609378 163318 1700000000000000000000000000000000000
TATATAAAAAATACTCAATATATA 2167	,	AGTITTAATAAGACTACTATGTATT 1549 	TCACAATAAACAAATCTATATCTAT 1489	AAAACGAACATAAAACTTATATTCT 2347	CTCTTTGTATAATTAATTTAT 1429	4; Length ; 132; Indels	DNA (Homo									4	with DWA Boolingt:								ATATTTTATATACACATTAAAAATAA 609319	60931	60937 1632 60931	1572 60937 1632 60931	1572 60937 1632 60931	1512 60943 1572 60937 1632 60931

Db 2166 ТТАТТАТАТАСТАЛАЛАЛАЛАСЛА 2144

Search completed: July 27, 2004, 04:23:19 Job time: 135 secs

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Minimum DB
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                   8:
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                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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1636
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Listing first 45 sv
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/cgn2_6/ptodata/2/pubpna/US09B_FUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                /cgn2
                                                                                                                                                                                                                                                                   6/ptodata/2/pubpna/US08 NEW PUB.seq:*
6/ptodata/2/pubpna/US08 PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

c 13	12	, 000	<b>1</b> 6 6 7	цαωд	Result No.
175 175	198 194.8	267.4	331.8 281.2	1042.4 420.2 375 369	Score
10.7	12.1	16.3	20.3	63.7 25.7 22.9	% Query Match
442 442	1333 1219 1479	1308	1168	5822 1631 1359	% Query Match Length
99	13	13	13	13 14 17	B B L
US-09-770-444-874 US-09-924-035A-369	US-10-424-599-61964 US-10-425-114-10970 US-10-424-599-141807	US-10-437-963-28561 US-10-425-114-30261 US-10-437-963-24606	US-09-782-130-26 US-09-782-130-26 US-10-260-238-618	US-10-437-963-24608	ID
Sequence 369, App Sequence 369, App	Sequence 61964, A Sequence 10970, A Seguence 141807	Sequence 28561, A Sequence 30261, A Sequence 24606, A	Sequence 24607, A Sequence 26, Appl Sequence 618, App	Sequence 1, Appli Sequence 1, Appli Sequence 24608, A	Description

<b>4</b> 5	44	43	42	41	40	. 9		37	36	35	34	LU LU	c 32		30	29	28	27	) N	200	24	23	22	12	220	19	18	· -	9 L	15
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•				•				7.5			7.8	7.9	8.0	٠	8.6					9.3	9.3				9.9	10.0	0			10.5
588	588	604	1723	1886	602	602	1605	588	565	2179	568	1248	746	589	1432	2012	1374	1067	1272	1185	1185	1472	596	811	1631	1984	~	785T	, ~	1673
17	17	17	17	17	17	17	17	17	13	17	17	16	9	17	13	13	17	13	17	11	9	13	17	16	13	13	13	Ŀ	1	13
-10-021-323	-10-021-323	-10-021-323-9998	-10-437-963-7302	-10-437-963	1-323-	-10-021-323-586	-10-437-963-	-10-021-323-973	-10-424-599-83	7-963-5661	-12	-238	-149-31	-323-592	5-11	-10-424-599-3362	-437-963-	-10	US-10-437-963-14307	US-09-938-842A-2520	8	-10-424-599-956	-10-021-323-985	0-260-238-339	-10-425-114-9	-10-424-599-9	0-424-599-5940	US-10-425-114-29325	-10-424-599-1167	US-10-362-091-3
9185,	Semience 5964 An	P GOOR	73025	e 31774.	n n	e 5860.	50404	9731,	Sequence 83751. A	56617	12	Sequence 498, App	31,	5922	7729. A	33624	43683	16916,	1430	(D No:	2520.	95670	9854	3398.	e 9445, r	e 92601.	e 59408.	N	<u>, , , , , , , , , , , , , , , , , , , </u>	Sequence 3, Appli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09924197 Publication No. US20030018993A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 5822
TYPE: DNA
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 Matches 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gutterson, Neal
APPLICANT: Oeller, Paul
TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
TITLE OF INVENTION: Repeat Sequences
FILE REFERENCE: 012176-0108100S
CURRENT APPLICATION NUMBER: US/09/924,197
CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/225,508
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 3
1499 CAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAAATTTAGTTGTTG
                                                                                    1439 CATGCAGATCTTCTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTT
                                                                                                                                                                 1379 TTAAAACCATGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTC
                        496 CAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTTAGTTGTTG 555
                                                                                                                                                                                                                       376
                                                                                                                   CATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGAAGCATCTAGTAAAATTT 495
                                                                                                                                                                                                         TTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTTCAGGTC 435
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                     63.7%;
99.4%;
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                                                                                                                                                                                                                                                        0; Gaps
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US-10-151-668-1

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GENERAL INFORMATION:
APPLICANT: ULVSKOV, Peter
APPLICANT: CHILD, Robin
APPLICANT: VAN ONCKELIN,
APPLICANT: VAN ONCKELIN,
APPLICANT: BORKHARDT, Bern
APPLICANT: SANDER, Lilli
                                                                                                                                                       Sequence 1, Application US/10151668 Publication No. US20020184660A1
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APPLICANT: BUNNGARD POULSEN, Gert
APPLICANT: BUNNGARD POULSEN,
APPLICANT: BOTTERMAN, Johan
TITLE OF INVENTION: Seed Shattering
FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/10/151,668
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/051,239
PRIOR APPLICATION NUMBER: US/09/051,239
PRIOR APPLICATION NUMBER: POT/EP96/04313
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR FILING DATE: 1995-10-08
PRIOR FILING DATE: 1995-12-08
NUMBER OF SEQ 1D NOS: 14
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LENGTH: 1631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1439)
OTHER INFORMATION: S
OTHER INFORMATION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE: INFORMATION: Location 95-163 = region encoding the OTHER INFORMATION: endo-PG signal peptide.

OTHER INFORMATION: Location 884 990 = region of the endo-OTHER INFORMATION: Corresponding to oligonucleotide PG3
OTHER INFORMATION: Location 1059-1073 = region of the endo-OTHER INFORMATION: Location 1059-1073 = region of the endo-OTHER INFORMATION: complementary to oligonucleotide PG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (95)...(1393)
LOCATION: (95)...(1393)
OTHER INFORMATION: Location 1229-1245 = region of the endo-PG
OTHER INFORMATION: complementary to oligonucleotide PG5
OTHER INFORMATION: Location 821-837 = region of endo-PG cDNA
OTHER INFORMATION: corresponding to oligonucleotide PG1.
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                                                         CATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATA
                                                                                                         TTGTTGATGGCAACGGAAATATCTGGTGGCAAAACTCATGCAAAATCGACAAATCTAAGC
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Pred. No. 1.4e-71;
0; Mismatches 383;
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US-10-437-963-24608
; Sequence 24608, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                      APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24608
LENGTH: 1359
TYPE: DNA
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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       ORGANISM: Oryza sativa
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Boukharov, Andrey
Barbazuk, Brad
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                                                                                             GGGCTACGCGAAGAACATCGTGTTCCAGAACATGATCATGGAAAATGTTTGGAACCCAAT
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RESULT 4
US-10-437-963-24607
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_29575C.1
US-10-437-963-24607
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Publication No. US20040123343A1
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LENGTH: 1182
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: AND EXPRESSION OF HETERO FILE REFERENCE: 16518.052
CURRENT APPLICATION NUMBER: US/09/782,130
CURRENT FILING DATE: 2001-02-12
CURRENT FILING DATE: 2001-02-12
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PRIOR FILING DATE: 1988-04-29
PRIOR APPLICATION NUMBER: US 07/168,190
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                                                  PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1988-03-15
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                NUMBER
                                 Remaining Prior Application data removed
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                                                                                                                               FILING DATE: 1985-01-17
APPLICATION NUMBER: US 07/582,241
FILING DATE: 1990-09-14
                                                                                                                                                                                           FILING DATE: 1993-08-10
APPLICATION NUMBER: US 07/526,123
FILING DATE: 1990-05-21
APPLICATION NUMBER: US 07/267,685
FILING DATE: 1988-11-02
APPLICATION NUMBER: US 06/692,605
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; ORGANISM: Lycopersicon
US-09-782-130-26
                                                                                                                             PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 618
LENGTH: 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 618, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
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SEQ ID NO 26
LENGTH: 2207
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APPLICANT:
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Best Local Similarity
Matches 342; Conservat
                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
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                               NAME/KEY: N_region
LOCATION: (8)..(8)
OTHER INFORMATION: n
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TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
                                                                               TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 60111-NP
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NAME/KEY: N_region
                       FEATURE:
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Goff, Stephen A.
Katagiri, Fumiyaki
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Briggs, Steven P.
Cooper, Bret
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Best Local Similarity
Matches 613; Conserv
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                               TTCATCGACACCGTGCACCTCTATGGCACCACCAATGGAGCTCGGATCAAGACATGGCAG
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TYPE: DNA
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APPLICANT: LA Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Best Local Similarity
Matches 607; Conserv
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Cao, Yongwei
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Boukharov, Andrey A.
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Pred. No. 4.8e-44;
); Mismatches 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                 GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                            Sequence 30261, Application US/10425114 Publication No. US20040034888A1
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 30261
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                                                                                                         AACAAAGGTGGCCATAAAATTTGATTGCAGCACAAACTTTCCATGTGAAGGAATTATAAT
                                                           GGAGAATAT 1288
                                                                                 TACCAAGGACGCCATCAAGATGAACTGCAGTGAGAACGTCCCATGCCAAGGCATTACCTT
                                                                                                                                     ACAAGAGTCAGCAGTGCAGGTCAGCGGTGTCGTCTTCAAGAACATTAGAGGGACGACCAG
                                                                                                                                                           ACAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAATATCAAGGGCACAAGTGC
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Pred. No. 5.9e-42;
0; Mismatches 326;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_29574C. US-10-437-963-24606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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ORGANISM: Oryza sativa
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TTTCCATGTGAAGGAATTATAATGGAGAATATAAATTT
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                                                 AAGAACATCAGGGGACAAGTGCATCAGAGGAGGCCATCGTGCTGCATTGCAGCAACAGT
                                                                                           GAGAATATCAAGGGCACAAGTGCAACAAGGTGGCCATAAAATTTGATTGCAGCACAAAC 1256
                                                                                                                                          GACTCTTCTACACCCTGCAAGCAACAGAAATCTGCAGTGGAGGTGAGCAATTTGCTGTTC
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Pred. No. 1.3e-34;
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RESULT 10
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APPLICANT: Cab Yongwei
APPLICANT: Cab Yongwei
APPLICANT: Cab Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 61964
LEEGTH: 1333
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Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT: Kovalic David K
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                                                                                                                                                                                                                  <u>AATCAGCATTGGAAGTCTAGGGAAAGACAACTCAACAGGCATAGTCACGAAAGTGATTTT</u>
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                               CATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGTATACAACAGTTTTCAGC
                                                                                                     ATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATGCAAGACGTTAAGTATCC
                                                                                                                                                                            AAATGAAGCCAAAATTATCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGCAGGGAGG
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CGGCTCGAGAGACCAATTTTACTGTGATTCTCCAACCAATTGTGAAAATCAGGCATCAGC
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 10970
LENGTH: 1219
TYPE: DNA
ORGANISM: Glycine max
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Publication No. US20040034888A1
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                             TAGGATCAAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTTCTGAATGT 108:
                                                                                                                                          AATTTATTGTGGACCAGGACATGGAATCAGCATTGGAAGTCTAGGGAAAGACAACTCAAC
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CAGAATTAAGACTTGGCAGGGAGGTTCTGGATATGTTCGAGGGGTGCGTTTTCAGAATGT
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Pred. No. 1.7e-28;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILS REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141807
LENGTH: 1479
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US-10-424-599-141807
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Best Local Similarity
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OTHER INFORMATION: Clone ID: PAT_MRT3847_99063C.1
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                                                            TGCAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAAT
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APPLICANT:
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APPLICANT:
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
                                                    APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
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                                                                                                                                                                                                                                                                              Ledford, Brooke L. Woessner, Jeffrey P. Haas, William David
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                                                                                                                                                                                    Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                                                   Matthew, Abraham V.
Ledford, Brooke L.
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Hamilton, Carol
Price, Jennifer
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                                                                                                                                                                                                                                                           Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                         Page, Amy
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PRIOR APPLICATION NUMBER: US 60/148,784;
PRIOR FILING DATE: 1999-08-13;
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 369
LENGTH: 442
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; TYPE: DNA
; ORGANISM: Arabidopsis
US-09-770-444-874
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Best Local S
Matches 275
                                                                                                                                                                                                                                                                                                                                            Sequence 369, Application US/09924035A Patent No. US20020142319A1 GENERAL INFORMATION:
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                                                               Matches 275;
                                                                                Best Local Similarity
                                                                                           Query Match
                                                                                                                                                                                                                                                     FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                                                     APPLICANT: Grlach, Jrn
TITLE OF INVENTION: Expressed Sequences
TITLE OF INVENTION: thaliana
                                                                                                                                      TYPE: DNA ORGANISM: Arabidopsis thaliana
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Local Similarity 65.0%;
les 275; Conservative
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                                  TCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTATCGGTGCCGAAAAT
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       TCAGAAGCATATGTTTCAAATGTGGTAGTCAACAAAGCGACTCTTATAGGAACCACTAAT
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Pred. No. 3.1e-24;
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US-10-362-091-3
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Publication No. US20040049809A1
GENERAL INFORMATION:
APPLICANT: Instituto de Cincia Aplicada e Tecnologia (ICAT)
TITLE OF INVENTION: Pear genes codifying for b-Galactosidase, P
TITLE OF INVENTION: Polygalacturonase, Expansin and their use.
FILE REFERENCE: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: PT 102511 C
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
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LOCATION: (112)...
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pyrus FEATURE:
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                                                                                                                                      TTGATGATCAATGCTTCAGCAAAGAGCCCCAAATACTGATGGAGTCCATGTATCAAATACT
                                                                                                                                                                                            CTAAACAGCCAAATGTTCCACATTGTCGTCAACGGCTGCCAAAATGTGAAAATGCAAGGT
TCTGGAGTCACCATTCTCGACTCCAAAATTTCAACCGGTGACGACTGTGTCTCAGTTGGC
                                           CAATATATTCAAATATCTGATACTATTATTGGAACAGGTGATGATTGTATTTCAATTGTT 878
                                                                                                GTCAAGGTTAACGCGGCCGGCAACAGCCCCAACACGGATGGCATCCATGTCCAAATGTCA
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Pred. No. 3.2e-23;
0; Mismatches 293;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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em_estpl:*
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gb_est1:*
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em_estfun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

	TITLE JOURNAL COMMENT	AUTHORS	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BM410796 LOCUS DEFINITION
Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute	Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002) Contact: CUGI	ALGAIA,J., VIREDALOV,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni I	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. bases 1 to 797)	Lycopersicon esculentum (tomato) Lycopersicon esculentum	cLEG54L15 5' end, mRNA sequence. BM410796 BM410796.1 GI:18262426	BM410796 797 bp mRNA linear BST 22-JAN-2002 EST585123 tomato breaker fruit Lycopersicon esculentum cDNA clone

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/note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1;
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/dev_stage="breaker"
/lab_host="SOLR"
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cLEG61A20 5' end, mRNA sequence-
BM412917
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://www.genome.clemson.edu/orders/index.html
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/dev_stage="breaker"
/lab_host="SOLR"
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  Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
Seq primer: T3.
                                                                                        Unpublished (2002)
Contact: CUGI
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                     Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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EST586855 tomato breaker fruit I
CLEG6014 5' end, mRNA sequence.
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  AGCTTCAAATTTGATGATCAATGCTTCAGCAAAGAGCCCCAAATACTG
                                                                                      TCTAAAGAGTAAAAATGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGT
                                                                                                                                      ATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAAATTTGAAAGTGAATAA
                                                                                                                                                                            ATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTGCAAAATTTGAAAGTGAATAA
                                                                                                                                                                                                                            TAGAAGGCTTTGGATTGCTTTTGATAGTTCAAAATTTAGTTGTTGGAGGAGGAGGAC
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/mol type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cla66014"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_bost="80LR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="tomato breaker recorded by the content of the content 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 3.7e-118;
0; Mismatches 1;
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REFERENCE
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JOURNAL
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Generation of ESTs from tomato fruit tissue, Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. I (bases 1 to 774)
1 (bases 1 to 774)
1 (bases 1, Urebalov, J., White, R., Vision, T., Karamycheva, S.A., Blcala, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM413004.1 GI:18264634
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                                                                                                                     CAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTA
                                                                                                                                                             CACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCAAATCACCTTTT
                                                                                                                                                                                   CACCTGTTCAATTTGTGGTTCCTAAAAACCAAGAATTATCTTCTCAAGCAAATCACCTTTT
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TTGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTGCA
                                                               AAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTAG
                                                                                                 CAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGAAGCATCTAGTA
                                   <u>AAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGTTCAAAATTTAG</u>
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmcUdadpt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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'cultivar="TA496"
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Pred. No. 3e-116;
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Generation of ESTs from tomato fruit tissue,
Unpublished (2002)
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100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATCAAGACTTTGGCAGGGAGGATCTGGACAAGCTAGCAAACATCAATTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATCAAGAC-TTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTG 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 742)
                                                                                                                                                                                                                       Location/Qualifiers
/tissue_type="Pericarp"
/dev_stage="breaker"
                                                        /clone="cLEG62H8"
                                                                                                                                                               organism="Lycopersicon"
                                                                                      db_xref="taxon:4081"
                                                                                                                /mol_type="mRNA"
/cultivar="TA496"
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RESULT 6
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BM413343
EST587670 tomato breaker fruit cLEG63C11 5' end, mRNA sequence
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                                                                                                                                                         CTTCAGCAAAGAGCCCAAATAC 793
                                                                                                                                                                                         AAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAATG
                                                                                                                                                                                                                        AAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTGATGATCAATG
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/clone lib="tomato breaker fruit"
/clone lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1;
/note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fru
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1 (bases 1 to 749)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giovannoni,J.
Generation of ESTs
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: CUGI
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CATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTTGCAAAAATTTGAAAGTGAATA
                                                                           CTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAG
                                                                                                                                                                                                                                                    CTATTTCAGTAAAGATTTTTGGATCCTTAGAAGCATCTAGTAAAATTTCAGACTACAAAG
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                                           primer:
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/rote="Vector: pBluescriptSKmCUadapt; Site 1: EcoR1;
Site 2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4081"
/clone="cLEG63C11"
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 728)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
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Generation of ESTs from tomato fruit tissue,
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    were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the perioarp."
                                                                              /clone lib="tomato breaker fruit"
/note="Yector: pBluescriptSKmCUadapt; Site_1: EcoR1;
/note="Yho1; supplier: Boyce Thompson Institute;
Site_2: Xho1; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 bp mRNA tomato breaker fruit Lycopersicon 5' end, mRNA sequence
                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="cLEG62K21"
                                                                                                                                                                                                                                                                 /organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                   /tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                lab_host="SOLR"
freezing the pericarp.
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                     Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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EST299068 tomato fruit red ripe,
                                                                                                                                                                  AW222257
                                                                                                                                                                                   clone cLEN7018,
                                                                                                                                                                                                                         AW222257
                                                                                                     Lycopersicon esculentum (tomato)
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Pred. No. 1.2e-111;
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5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giovannoni, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                         ACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTTCACTA
                                                                                                       GAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAAGTGGAAAACCATCAGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAACAGGTGATGATTGTATTTCAATTGTTTCTGGATCTCAAAATGTGCAGGCCACAA
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                                                                                 GAAGGAATTATAATGGAGAATATAAATTTAGTAGGGGAAAGTGGAAAACCATCAGAGGCT
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ACGTGCAAAAATGTCCATTTTAACAATGCTGAACATGTTACACCACACTGCACTTCACTA
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/Glone libe "tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
"toward and "toward and "toward and "toward and "
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/dev_stage="red_ripe_(7-20_days_post-breaker)"
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/clone="cleN7018"
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/cultivar="TA496"
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Pred. No. 9.7e-109;
0; Mismatches 5;
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Generation of ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
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EST311335 tomato fruit red ripe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.genome.clemson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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TGCACAACAAATTCATATCAAATTTGAGTCATGCACTAATGTTGTAGCTTCAAATTTTGAT
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                                                  Conservative
                                                                                                                                                                          /tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone_lib="tomato fruit red ripe, TAMU"
/clone_lib="tomato fruit red ripe, TSM(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe), 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
discarded. Fruit were cut in half and the seeds and
                                                                                                                                                          locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/clone="cLEN19E19"
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                                                                  43.2%;
99.9%;
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                                                Score 707.4;
Pred. No. 1.8e
0; Mismatches
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1.8e-108;
-hag 1;
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764 GATCAATGCTTCAGCAAAGAGCCCAAATACTGATGGAGTCCATGTATCAAATACTCAATA 823

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                                                                                                                        Giovannoni, J.
Generation of ESTs from
Generation (1999)
                                                                                Contact: CUGI
Clemson University Genomics Institute
Clemson University
                                             Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                                                                                                      1 (bases 1 to 696)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                   AW442253 696 bp mRNA linear EST 18-MAY-200: EST311649 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
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AW442253.1 GI:6977504
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                                                                         Jordan Hall, Clemson, SC 29634, USA
/organism="Lycopersicon esculentum"
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                                                              TCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGC
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Best Local Similarity
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TCGGTGCCGAAAATGGAGTTAGGATCAAGACTTGGC
                                                                                                    TAGGATCTGGAAATTCAGAAGCTTATGTGTCTAATGTTACTGTAAATGAAGCCAAAATTA 1008
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/cultivar="TMA96"
/db_xref="taxon:4081"
/dlone="clEN22G14"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone lib="comato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
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Pred. No. 2.7e-106;
0; Mismatches 1;
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1 (bases 1 to 687)
1 (brach,J., Wansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Romning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
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AW442335.1 GI:6977586
EST.
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EST311731 tomato fruit red ripe, T
clone cLEN22L13 5', mRNA sequence.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="red ripe (7-20 days post-breaker)"
/clone lib="tomato fruit red ripe, TAMU"
/clone lib="tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/not; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="pericarp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="TA496"
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99.7%;
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                                                                                                                                                                                                                                                                                                   primer: T3
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/clone="cLEG71124"
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Ewkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 703)
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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Generation of ESTs from tomato fruit tissue, breaker stage (2002)
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/clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSMcUWadapt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                             /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
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                                                                                                                                                                        Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                          l (bases 1 to 677)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,T.E., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                            AW442241
EST311637 tomato fruit red ripe, T
                                                      Giovannoni, J.
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AW442241.1 GI:6977492
EST.
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Pred. No. 6.8e-103;
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                                 fruit tissue
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Clemson University Genomics Institute
Clemson University
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AGTGCAACAAAGGTGGCCATAAAATTTGATTGCAGCACAAAACTTTCCATGTGAAGGAATT
                                                                                                    ATACAACAGTTTTCAGCAGTTCAAGTGAAAAATGTGGTGTATGAGAAATATCAAGGGCACA 1214
                                                                                                                                                                                                         CAAGACGTTAAGTATCCCATAATTATAGACCAAAACTATTGTGATCGAGTTGAACCATGT
                                                                                                                                                                                                                                                                                                      AAGACTTGGCAGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATG
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                                                                                                                                                                                                                                                                               AAGACTTGGCAGGGAGGATCTGGACAAGCTAGCAACATCAAATTTCTGAATGTGGAAATG
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                                                                             {	t ATACAACAGTTTTCAGCAGTTCAAGTGAAAAATTGTGGTGTATGAGAATATCAAGGGCACA}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone libe"tomato fruit red ripe, TAMU"
/clone libe"tomato fruit red ripe, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; supplier: Giovannoni, Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
blossom end of the fruit) and harvested 7 days
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/cultivar="TA496"
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Matches 672;
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100 Jordan Hall, Clemson, SC 29634, USA
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
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Generation of ESTs from tomato fruit tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
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EST582873 tomato breaker fruit
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                                                                                                                                                                                                                                          TTCATCTAGAACACCTGTTCAATTTGTGGTTCCTAAAAACAAGAATTATCTTCTCAAGCA
                                                                                                                                                               AATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTTGGATCCTTAGA
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                      TCAAAATTTAGTTGGAGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCC
                                                                                                 AGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGT
                                                                                                                                        AATCACCTTTTCAGGTCCATGCAGATCTTCTATTTCAGTAAAGATTTTTGGATCCTTAGA
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                                                             AGCATCTAGTAAAATTTCAGACTACAAAGATAGAAGGCTTTGGATTGCTTTTGATAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fru
                                                                                                                                                                                                                                                                                                                                                                                           were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/lab_host="SOLR"
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/cultivar="TA496"
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'clone="cLEG45C7"
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Generation of ESTs
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                                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: CUGI
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                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
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Matches 662; Conservative
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                                                CAAAAATTTG 677
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CAMATATTTG 670
                                                                                                  CAAAATAAATAAATCACTGCCATGCAGGGATGCACCAACGGCCTTAACCTTCTGGAATTG
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                                                                                                                                                                                                                                   AGTTGTTGGAGGAGGAACTATCAATGGCAATGGACAAGTATGGTGGCCAAGTTCTTG 607
                                                                                                                                                                                                                                                                                                   TAGAATTTCAGACTACAAAGATAGAAAGCTTTTGGATTGCTTTTGATAGTGTTCAAAATTT
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/note="Vector: pBluescriptSKmcUadapt; Site 1: EcoR1;
Site 2: XhoI, supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
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Search completed: July 27, 2004, 02:46:01 Job time: 4445 secs

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MANAGARIA	AKIIGAENGVR             AKIIGAENGVR	QYIQISDTI          QYIQISDTI	WWPSSCKINKSLPCRDAPTALIFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMIN	lkqitfsgpcrssisvkifgsleasskisdykdrrlwiafdsvonlvvggggtingngq 	ಬ — ಬ	$\frac{\text{SI}}{\text{SI}}$	0%; Score 0%; Pred. 0; Mist	US-0 US-0 US-0 US-0 US-0 US-0 US-0 US-0
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TVENCE SOCIETIES	GGSGQASNI           GGSGQASNI	ISIVSGS(	NLKSKNA(	DRRLWIAI         DRRLWIAI	TAFEQAWI         TAFEQAWI	KQVYDNIL	DB 6; .8e-208; s 0;	2-49 2-47 2-67 2-51 2-51 2-51 2-71 2-73 2-73 2-74 2-2-8 2-2-8 2-2-8 2-2-8 1-10 1-10 1-10 1-10 1-10 1-10 1-10 1-
THE DOES	SGQASNIKFLNVEMQ             SGQASNIKFLNVEMQ	ONVOATNI          ONVOATNI	001H1KFE	TINOVSCE           	VEACSSRTPV            VEACSSRTPV	EQEFAHD	Length : Indels	NOD
TAMENTA	DVKYP       	IVSGSQNVQATNITCGPGHGISIGS	THIKFESCTNVVASNLMIN	VQNLVVGGGGTINGNGQ	OFVV OFVV	AHDFQAYLSY           AHDFQAYLSY	457;	TTP TTP TTP TTP TTP TTP TTP TTP
TUCESO	NOON IDON IDON	H—H		<<	PKNKNYL 	AYLSYLSKNIE (	Gaps	49, Ap 47, Ap 48, Ap 51, Ap 51, Ap 713, Ap 713, Ap 714, Ap 26, Ap 9, Ap 10, Ap 10, Ap 10, Ap 10, Ap
3	360 360	300	240 240	180 180	120 120	60	0;	

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RESULT 2
US-09-051-239A-2
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Best Local S
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SEQ ID NO 2
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Patent No. 6420628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/EP96/04313
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR FILING DATE: 1995-10-06
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR FILING DATE: 1995-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/09/051,239A
CURRENT FILING DATE: 1998-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOTTERMAN, Johan TITLE OF INVENTION: Seed Shattering FILE REFERENCE: 2121-0138P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                   IIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINL 415
                                                                                                                                                                            NLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGI
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BORKHARDT, Ber
SANDER, Lilli
IIDQNYCDK-DKCEQQESAVQVNNVVYQNIKGTSATDVAIMENCSVKYPCQGIVLENVNI
                                                                                 SIGSLGDDNSKAYVSGIDVDGATLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPI
                                                                                                                   SIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPI
                                                                                                                                                         NVKITAPGDSPNTDGIHIVATKNIRISNSDIGTGDDCISIEDGSQNVQINDLTCGPGHGI
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                                                                                                                                                                                                                                                          GNGQVWWDSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVAS
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                                                                                                                                                                                                                                                                                                                                                 YLLKQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVFLCVLLMLACCQALSSNV-DDG------YGHEDG---SFESDSLIKLNNDD
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BUNDGARD POULSEN, Gert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1113; DB 4;
Pred. No. 2.2e-92;
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Mismatches 121;
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US-08-941-532-6
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                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 950
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: BECOME BOACKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROBERTS, Jeremy Alan
APPLICANT: COUPE, Simon Allan
APPLICANT: JENKINS, Elizabeth Sarah
TITLE OF INVENTION: CONTROL OF POD
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 Local Sin hes 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                         KIWWQNSCKIDKSKPCTKAPTALTLYNLNNLNVKNLRVRNAQQIQISIEKCNSVDVKNVK 234
                                                                                                                                   KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG 178
                                                                                                                                                                            S-----TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLIPKGKTYLL 114
                                                                                                                                                                                                                                                      AIFLCVLLMLACCQALSSNVDDGYGHEDGSFET--DSLIKLNNDDDVLTLKSSDRPTTES
                                                                                                                                                                                                                                                                                            SILLLIIIFASSISTCRSNVID-----DNLFKQVYDNILEQEFAHDFQAYLSYLSKNIES 61
                                                           QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM 238
                                                                                                   KSIRFRGPCKSLRSFQILGTLSASTKRSDYSNDKNHWLILEDVNNLSIDGGSAGIVDGNG 174
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RESULT 4
US-08-467-023-134
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                                 Query Match
Best Local Similarity
Matches 168; Conserv
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                              REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulogic Pharmaceutical Corporation,
STREET: 610 Lincoln St
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/ACENT INFORMATION:
NAME: Jame B. Remillard
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 6, CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergen
TITLE OF INVENTION: Japanese
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                                                                                                                                                                    LENGIH:
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                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
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AHDFQAYL ---
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                                                                                                                                                                    514 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bond, Julian F.;
Garman, Richard D;
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuo, Mei-Chang;
Yeung, Siu-mei H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pollock,
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                                                                                                                                                                                                                                                                                                                                                                                                      June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allergenic Proteins And Peptides From 
Japanese Cedar Pollen
: 261
 -SYLSKNIESNNNIDKVD---KNGIKVINVLSFGAKGDGKTYDNIAFEQA
                                                 32.9%;
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                                   73;
                                                                                                                                                                                                                                                                      025.6 USD2 (IMI-028CPD2)
                                 Score 787; DB 3;
Pred. No. 9.1e-63;
3; Mismatches 160
                                   160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1.25
                                                               Length 514;
                                   Indels
                                   14;
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RESULT 5
5453566-2
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                                                                                                                                    US-08-467-023-189
                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHEWMAKER, CHRISTINE K.; KRIDL, WILLIAM R.; KNAUF, VIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IN PLANT/CELLS
                                                                                                Sequence 189, Application US/08467023 Patent No. 6090386
                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                 GENERAL INFORMATION:
                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 27-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     applicant: SHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 240,408
FILING DATE: 30-AUG-1988
APPLICATION NUMBER: 920,574
FILING DATE: 17-OCT-1986
APPLICATION NUMBER: 845,676
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTISENSE REGULATION OF GENE EXPRESSION
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 SKNAQQIHIKFESCINVVASNLMINASAKSPNIDGVHVSNIQYIQISDIIIGIGDDCISI
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                                                                                                                                                                                                         61 SSISVKIFGS
                                                                                                                                                                                                                                                                                                      72 GIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 WQAACKNPS-AMLLVPGSKKFVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 WNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWI 158
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                                                                                                                                                                                                                                                                                                                                              15.3%; Soilarity 100.0%; For Conservative 0;
Garman, Richard
Kuo, Mei-Chang;
                                               Griffeth, Irwin Pollock, Joanne;
                                Bond, Julian F.;
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                                                                 Irwin J.;
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                                                                                                                                                                                                                                                                                                                                                                               Length 70
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RESULT 7
US-09-107-532A-6652
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                                                                                                                                                                                                 Sequence 6652, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350
PILING DATE: December 6, 1
PILING DATE: DECEMBER: 6, 1
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Allergenic Proteins And Peptides TITLE OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995
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CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 HGISIGSIGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVK 352
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                                                    COUNTRY: USA
ZIP: 02354
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                                                                                               STATE: Massachusetts
                                                                                                                   CITY: Waltham
                                                                                                                                       STREET: 100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeung, Siu-mei
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internal
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ER: 025.6 USD2 (IMI-028CPD2)
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AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAF
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                                                                                                               RESULT 8
US-08-290-978A-5
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        Sequence 5, Application US/08290978A
Patent No. 5624834
GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN, MARGO
APPLICANT: MULLER, YVONNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...451
SEQUENCE DESCRIPTION: SEQ ID NO: 6652:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       228
                                                                                                                                                                                                    344 HASA 347
                                                                                                                                                                                                                                           386 KGTS 389
                                                                                                                                                                                                                                                                                                                             341 IKFLNVEMQDVKYPIIIDQNY-CD--RVEPCIQQ--
                                                                                                                                                                                                                                                                                                                                                                                                          282 VQATNITCGPGH-GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 NGKKWWHTFRNEPD----NLAYP---RPKLMSFHNCHRITVKDIKLIQSPSWTINPILCS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 NVVASNIMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGS------QN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 SISVKIFGSLEASSKIS-DYKD------RRLW---IAFDSVQNLVVGGGGTING 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 KSNVELHLSAGAVLKFSDDPKDYPVVHSRWEGVHRKVYASCIYAQNVENISVTGFGTLDG 114
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                                                                                                                                                                                                                                                                                        IRVSNIVMDNVMCPFILNLYYFCGPRGKEPYVWEKKAYPIDERTPAFRRIHFSNITARNV 343
                                                                                                                                                                                                                                                                                                                                                                     ITITNCTMVHGHGGVVLGSEMSGS----IRNITISNCIFQETDRGIRLKSRRGRGGIVED 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATFDNLTILNPADSPNTDGIDPESCKNVRISNCHIDVGDDCIAIKAGTEDTYERIACEN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGQVWW-----PSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENGTH: 451 amino acids
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Length 451; Indels

68;

Gaps

15;

FSAVQVKNVVYENI 385

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443 LSVNCTA 449

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US-08-290-978A-5
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Best Local :
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TELEFAX: (202) 887-0763
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CLASSIFICATION: 435
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VIPHCIS
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                                                                                                                                                                                                                                                                                                                                                                                                                             WPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKNIDLEVLGTILFTNDTDYWQANSFKQGFQNATTFFQLGG-EDVNMYGGGTINGNGQVW
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                                            RGTTSGSEDPYVGTIV---
                                                                                                                        ADLQGGGGSGSVKNITYDTALIDNVDWAIEITQCYGQKNTTLCNEYPSSLTISDVHIKNF
                                                                                                                                                                  -----GGSGQASNIKFLNVEMQDVKYPIIIDQNYCDR-VEPCIQQFSAVQVKNVVYENI 385
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  444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 298.5; DB 1; 25.1%; Pred. No. 1.3e-18; ative 73; Mismatches 166;
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                                                                                  TKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEH 437
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                                        CSSPDTCSDIYTSNINVTSPDG-TNDFVCDNV---DESL
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                                                                                                                                                                                                                                                                                                    Matches 107;
                                                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 17-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                     Match 12.5%;
Local Similarity 25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MURASHIGE, KATE REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                 212 YSKSDNEAKNIDGWDIYRSNNIVIQNSVINNGDDCVSFKPNSINILVQNLHCNGSHGISV
                                                                                                                                                                                                    131 RSSISVKIFGSL-----EASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVW 181
                                                                                                                                                                     97 LKNIDLEVLGTILFTNDTDYWQANSFKQGFQNATTFFQLGG-EDVNMYGGGTINGNGQVW
                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                  74 KVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL---KQITESGPC 130
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     GSLGSGNSE---
                                                                  SAKS----PNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISI 297
                                                                                                   YDLYAEDDLIL----RPILMGIIGLNGGTIGPLKLRYSPQYYHFVANSSNVLFDGIDISG
                                                                                                                                  WPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                      452 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAN OOYEN, ALBERT J.J
ROLIN, CLAUS
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUSTERS-VAN SOMEREN, MARGO
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                                                                                                                                                                                                                                                                                                    Score 298.5; DB 2;
Pred. No. 1.3e-18;
3; Mismatches 166;
                                                                                                                                                                                                                                       ---CNHGGKVVF--DEDKEYIIGTALNMTF----
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                                                                                                                                                                                                                                                                                                                                     Length 452;
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; ORGANISM: Aspergillus tubingensis
US-09-787-583-2
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PRIOR APPLICATION NUMBER: EP 99200481.2
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: EP 98203171.8
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vorägen, Alphons
TITLE OF INVENTION: ASPERGILLUS TUBIGENSIS POLYGALACTURONASE
FILE REFERENCE: 24615-20144.00
CURRENT APPLICATION NUMBER: US/09/787,583
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
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                                                                                                                          318 SSGTDIYIL--CGSG-SCSNWTWSGVDVTG--GKKS-SKCKNV 354
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                                                                                                                                                                TSATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNV 430
                                                                                                                                                                                                        YGKTGTVENVKFEDITLSDISKYGIVVEQDY-ENGSPTGTPTNGVKVEDITFKKVTGSVK
                                                                                                                                                                                                                                                                                                                             CISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTW 331
                                                                                                                                                                                                                                                                                                                                                                                                           QQIHIKFESCTNVVASNLMIN-----ASAKSPNTDGVHVSNTQYIQISDTIIGTGDD
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Meeuwsen, Petrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ooijen, Albert
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Pred. No. 2.6
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nes 91;
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US-08-061-062A-6
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CURRENT FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: PA 1999 00390
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 60/125,884
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: PCT/DK00/00136
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SOFTWARE: PatentIn vers
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APPLICANT: Kristensen, Henrik
TITLE OF INVENTION: An Enzymatic Treatment Method
FILE REFERENCE: 5871.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-22
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ORGANISM: Trichisporon
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                               APPLICANT: VERBAKEL, Johannes M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA
TITLE OF INVENTION: ENCODING A RIPENING FORM OF A
TITLE OF INVENTION: RHAMNOGALACTURONASE ACTIVITY
NUMBER OF SEQUENCES: 16
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APPLICANT:
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                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                  ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
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  APPLICATION NUMBER:
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                                                                                                                                                                                 WASHINGTON,
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                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           STAM, HEIN
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US/08/061,062A
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                                          Version
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Length 360; Indels

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Best Local Similarity 24.0
                                                                                                                                                                                                                                                                                               Patent No. 5550045
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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LENGTH: 440 amino acid
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NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            APPLICANT: VERBAKEL, Johannes M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA
TITLE OF INVENTION: ENCODING A RIBENING FORM OF A POLYPEPTIDE HAVING
TITLE OF INVENTION: RHAMMOGALACTURONASE ACTIVITY
                                                                                                                                                                                                                                                                    APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Disk
                                                                                                                         NUMBER OF SEQUENCES: 1
                                ZIP:
                                                                  ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON, D.C.
                                  COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       366
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                                                                                                                                                                                                                                      VISSER,
                                                                                                                                                                                                                                                     SUYKERBUYK, MARIA E
                                                                                                                                                                                                                                                                    STAM, HEIN
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                                                                                                                                                                                                                                  JACOB
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RESULT 14
US-08-536-150-6
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                                                                                                                                                                                                                                           Sequence 6, Application US/08536150 Patent No. 6013489
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Best Local
                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14 MAY 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 2
                                 TITLE OF INVENTION: CLO
TITLE OF INVENTION: ENC
TITLE OF INVENTION: RHA
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 440 amino acid
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ADDRESSEE:
STREET: 11
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TELEPAX: (202) 822-0944
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1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                    MUSTERS, WO
                                                                        VERBAKEL, JOHANNES M.
VENTION: CLONING AND EXPRESSION OF DNA
VENTION: ENCODING A RIPENING FORM OF A
VENTION: RHAMNOGALACTURONASE ACTIVITY
                                                                                                                                                 VISSER, JACOB
                                                                                                                                                                  SUYKERBUYK, MARIA E.
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Pred. No. 2e-13;
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129 11;

COUNTRY:

WASHINGTON,

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                                                                                                                                             RESULT 15
                                                       Sequence 8, Application US/08536150
Patent No. 6013489
GENERAL INFORMATION:
APPLICANT: MUSTERS, WOUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/061,062 FILING DATE: 14 MAY 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 29-SEP-1995
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                                                                                                                                                                                                                                                                                                                                             250
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                                                                                                                                                                                                                                    ATCKNVH 431
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                                                                                                                                                                                                                                                                     A---GDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSEL 365
                                                                                                                                                                                                                                                                                                     CIQQFSAVQVKNVVYENIKGT---SATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSE
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MUSTERS, WOUTER
STAM, HEIN
SUYKERBUYK, MARI
VISSER, JACOB
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Pred. No. 2e-13;
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 8
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TITLE OF INVENTION: (
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KOKILIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/061,062
FILING DATE: 14 MAY 1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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CTTY: WASHINGTON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.1%; Score 241; DB 3 Local Similarity 24.0%; Pred. No. 2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 29-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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366 YLCRSAY 372
                                          425 ATCKNVH 431
                                                                                                                                                                           250 DVTDIVYRNVYTWSSNQMYMIKS-NGGSGTVSNVLLENFIGHGNAYSLDIDGYWSSMTAV 308
                                                                                                                                                                                                                     308 YVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEP 367
                                                                                                                                                                                                                                                                      194 LDGIDVWGSN-IWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCAMGSLG---ADT 249
                                                                                                                                                                                                                                                                                                                                                             144 GARILRLTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 CRSSISVK--IFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCK 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
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INVENTION: CLONING AND EXPRESSION OF DNA
INVENTION: ENCODING A RIPENING FORM OF A POLYPEPTIDE HAVING
INVENTION: RHAMNOGALACTURONASE ACTIVITY
                                                                                    A---GDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSEL 365
                                                                                                                                CIQQFSAVQVKNVVYENIKGT---SATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSE 424
                                                                                                                                                                                                                                                                                                              TDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEA 307
                                                                                                                                                                                                                                                                                                                                                                                                       INKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SATAIQLDGIIYRTGTASGNMIAVTDTTDFELFSSTSK-----GAVQGFGYVYHAEGTY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGATKTCNILSYGAVADNSTDVGPAITSAW-AACKSGGLV--YIPSGNYALNTWVTLTGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 amino acids
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Job time : 29.379 secs

Page 9

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-018-604-2
2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  July 21, 2004, 17:08:27 ; Search time 79.2655 Seconds (without alignments) 1802.048 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1285356 segs, 312560742 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published
// Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
// Cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US06_REW_PUB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
// Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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// Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

15	14	13	12	11	10	9	8	7	o.	υī	4	Ų		۲	Result
701.5	723.5	724.5	728	728	734	739	785	787.5	808	870	988.5	1010	1011	1113	Score
29.4	30.3	30.3	30.5	30.5	30.7	30.9	32.8	32.9	33.8	36.4	41.4	42.3	42.3	46.6	Query Match Length DB
400	492	398	456	443	503	485	534	514	508	319	444	452	393	433	ength
16	12	12	12	12	16	16	16	10	16	12	16	16	16	13	1
US-10-437-963-155040	US-10-424-599-284649	US-10-362-091-4	US-10-425-114-44707	US-10-424-599-235443	US-10-437-963-172689	US-10-437-963-175508	US-10-437-963-134257	US-09-847-208-69	US-10-437-963-154485	US-10-425-114-69361	US-10-437-963-131044	US-10-437-963-127091	US-10-437-963-127090	US-10-151-668-2	HD
Sequence 155040,	Sequence 284649,	Sequence 4, Appli	Sequence 44707, A	Sequence 235443,	Sequence 172689,	Sequence 175508,	Sequence 134257,	Sequence 69, Appl	Sequence 154485,	Sequence 69361, A	Sequence 131044,	Sequence 127091,	Sequence 127090,	Sequence 2, Appli	Description

Length 433;

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12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	16	12	16	16	12	12	12	12	12	16	16	16	16	12	7
-10-425-114-727	-10-425-114-6556	0-425-114-6451	-10-425-114-54	-10-425-114-4680	0-425-114-567	-10-425-114-5298	-10-425-114-4680	-10-425-114-4648	-10-425-114-655	-425-114-6453	-10-425-114-6295	-10-425-114-384	-10-425-114-5098	-10-424-599-17646	-10-437-963-110	-10-424-599-20480	-10-437-963-12708	0-437-963-11017	-10-425-114-5	0-425-114-3847	-10-425-114-4198	-10-424-599-17632	-10-424-599-2385	-10-437-963-11611	37-963-14616	0-437-963-16235	0-437-963-15910	0-425-114-6615	TRCE-STI-C25-0
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## ALIGNMENTS

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; OTHER INFORMATION: Strain cv. US-10-151-668-2
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US-10-151-668-2
                                                                                                                                                                                                                                             TITLE OF INVENTION: Seed Shattering
FILE REFERENCE: 2121-0138P
CURRENT APPLICATION NUMBER: US/10/151,668
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/051,239
PRIOR FILING DATE: 1998-09-28
PRIOR PELICATION NUMBER: PCT/EP96/04313
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR APPLICATION NUMBER: EP 95 402241.4
PRIOR APPLICATION NUMBER: EP 95 203328.0
PRIOR APPLICATION NUMBER: EP 95 203328.0
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APPLICANT: CHILD, RO
APPLICANT: VAN ONCKI
APPLICANT: PRINSEN,
                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Publication No. US20020184660A1
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                           PRIOR FILING DATE: 1995-12-08
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                             TYPE: PRT
ORGANISM: Brassica
                                                                                               FEATURE:
                                                                                                                                                     LENGTH: 433
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BUNDGARD POULSEN,
BOTTERMAN, Johan
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SANDER, Lilli
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 46.6%;
49.9%;
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 Score 1113; DB 13; Pred. No. 1.8e-97;
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US-10-437-963-127090
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 127090
LENGTH: 393
                                                                                                                                                         Query Match
Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 127090, Application US/10437963 Publication No. US20040123343A1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                              SSISVKIFGSLEASSKISDYKDR--RLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKIN
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                                                                             GSNVFSIQSYGAHGDGRHDDTKALGDTWAAACSSAKPAVLLIPKGKKYLIKHTTLSGPCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILLLIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNID
    SSISLMVKGSLVASPERSDWSKETIRHWILISGVTGLTVTGGGTIDGNGKIWWQNSCKTN
                                                                                                                  GIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGSLGDDNSKAYVSGIDVDGATLSETDNGVRIKTYQGGSGTAKNIKFQNIRMDNVKNPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVFLCVLLMLACCQALSSNV-DDG-
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                                                                                                                                                       42.3%; Score 1011; DB 16; Length 53.3%; Pred. No. 9e-88; vative 57; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrey A.
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_29576C.1.pep
US-10-437-963-127091
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; Sequence 127091, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 127091
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Best Local Similarity
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APPLICANT:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                   SVKIFGSLEASSKISDYKDR--RLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSL 192
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                                                                                                                                                                                                                                                                                                                                       TEMIEGTLVAPPKRSDWSKETIRHWIMFNGVSGLTVAGGGGTVDENGKIWWQNSCKTNAKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   VINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTFVQFVVPKNKNYLLKQITFSGPCRSSI 134
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                      SAVQVSNVVFKNIRGTSASKEAIKLDCSRNVPCQGITLKDVKLTIKGG
                                                         SAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESG
                                                                                                                                      TVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQF 372
                                                                                                                                                                             ITRSKNVQVTGCIIKTGDDCMSIEDGTENLHVKNMVCGPGHGISIGSLGDHNSEAHVNNV
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                                                                                                    TVDTVRLYGTTNGARIKTWQGGWGYAKNIVFQNMIMENVWNPIIIDQNYCDSATPCKEQT
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Barbazuk, Brad
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Cao, Yongwei
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54.6%;
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With

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RESULT 5
US-10-425-114-69361
; Sequence 69361, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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US-10-437-963-131044
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Xoxalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
APPLICANT: Tabaska, Jack
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclei
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Publication No. US20040123343A1
GENERAL INFORMATION:
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SEQ ID NO 131044
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Best Local :
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 VINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                    Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                   TVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPC-IQQ
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                                                                                                                                                                                                                                                          AKWRKSGTVVPQPCTS
                                                                                                                                                                                                                                                                                               VHFNNAEHVTPH-CTS
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                                                                                                                                                                                                                                                                                                                                                                      FSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINL--VGESGKPSEATCKN
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Cao, 1
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Li, Ping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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 Nucleic
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49.5%;
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     Acid
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Pred. No. 1.5e-85;
     Molecules
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   and Other
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   Molecules
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     Associated
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                                                                                    US-10-437-963-154485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-154485
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Plants and Uses There
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 69361
LENGTH: 319
                                                                                                                                                                   SEQ ID NO 154485
LENGTH: 508
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154485, Application US/10437963 Publication No. US20040123343A1
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                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                       Query Match
                                                                                                                                                                                                                               APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
CURRENT FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: UC-ZMFLB73002C03_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                        OTHER INFORMATION:
                                                                                                                           FEATURE:
                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 NAKWTEFGTVRPQPCTAIK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SGITIDSVQLHGTTNGARIKTYQGGSGYAKDITFQNMVMYDVKNPIIIDQNYCDKAKPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GIHITRSKDVRVTDCKIKTGDDCMSIENGTHNLHVSKVNCGPGHGISIGSLGDDNSRAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 GVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 KSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 SSISVKIFGSLEASSKISDY--KDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKIN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSVTLTVKGTLVASPNRADWSDNDRRHWIVFRSIDKLTVNGGGAIDGNGEKWWPHSCKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQESAVQVSGVVFKNIRGITSTKDAIKMNCSENVPCQGITLQNIDLKMQDGKGNTRSTCQ
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  Conservative
                                                                                                     Clone ID: PAT_MRT4530_54340C.1.pep
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33.8%; Score 808; DB 16; 36.4%; Pred. No. 3.6e-68; tive 91; Mismatches 167;
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Pred. No. 2.1e-74;
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    167;
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                                       Length 508;
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    44;
    Gaps
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US-09-847-208-69
Sequence 69, Application US/09847208
Publication No. US20030082190A1
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                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Cryptomeria japonica (Japanese cedar)
US-09-847-208-69
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Best Local
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LENGTH: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES FILE REFERENCE: UC67.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Saxon, Andrew APPLICANT: Zhang, Ke APPLICANT: Zhu, Daocheng
                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 173; Conserv
                                                                                 107
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                                                                               FFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGVIDGQGKQWWAG 166
                                   SCK-INKSLPC--RDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
                                                                                                                     TFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS
                                                                                                                                                           VEHSRHDAINIFNVEKYGÄVGDGKHDCTEAFSTAWQAÄC-KKPSAMLLVPGNKKFVVNNL
                                                                                                                                                                                                  VD---KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI
                                                                                                                                                                                                                                          VAMQLIIMAAA---
                                                                                                                                                                                                                                                                                  ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFDCSTNFPCEGIIMENINLVGESGKPSEATCKN--VHFNNAEHVTPHCTSLEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDY--KDRR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSKNIESNNNIDKVDKN---
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  QCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLACSDAVPCVGIVLSDIDLRREDGGGEVQTVCNCAMGFDDG-RVSPAADCLRTS 482
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                                                                                                                                                                                                                                                                                                                      Score 787.5; DB 10; Pred. No. 3.3e-66; 8; Mismatches 163;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_36049C.1.
US-10-437-963-134257
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SEQ ID NO 134257
LENGTH: 534
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  141 SLEASSKISDY--KDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCR--D 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 FGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFG 140
                                                                                                                                                                                                                     QYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNE 316
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Boukharov, Andr
Barbazuk, Brad
                    SLKLGNFSSLWMQTQAVEVRKIEFAGIRGTSATEQAIKLACSDAVPCRDLELRNVNLTMV
                                                                                                                                        AKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVEPCIQQ-----
                                                                                                                                                                                                                                                                                                     APTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNT 256
                                                                                                                                                                                                                                                                                                                                                                                                                            FGAVGDGITNDTQAFLDAWNAACASTEPAVLAVPAGKTYQIWPVRLAGPCKKKLKLMISG
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                                                      -----PS-----AVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                  CLLTNTTNGVRİKSWQGGMGYAHNLRFEGIVMKNVSNPİIIDQYYCDQPTPCANQSTSSS
                                                                                                                                                                                THAQIMDNLISTGDDCVSMVGNCSDVRVKDISCGPGHGISIGSLGKNRTTDRIENVRVDT 369
                                                                                                                                                                                                                                                               APKALQFEECRRVSVQGITMQNGPQFHLMFTRCTDVKASFLRVVAPESSPNTDGIHLNDT 309
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77; Mismatches 146; Indels
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Pred. No. 6.1e-66;
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Length 534;

22;

Gaps

189

249

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SGKPSEATCKNVHENNAEHVTP

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APPLICANT: Li, Pring

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

SEQ ID NO 175508

LENGTH: Acc
                                                                                                                                               RESULT 10

US-10-437-963-172689

; Sequence 172689, Application US/10437963

; Publication No. US20040123343A1
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US-10-437-963-175508
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Best Local S
Matches 153
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                                                                                                                             GENERAL INFORMATION:
              APPLICANT:
                                                                    APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT:
                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VFQVDGVLMPPDGPDCWPPSDNRRQWLVFSNLDGLTLRGAGTIEGNGEGWWNLPCKPHRG
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                                      Zhou, rim
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Wu, Wei
Barbazuk,
              Boukharov,
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                Andrey A.
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; Pred. No. 1.3e-61;
62; Mismatches 128;
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                                                     ; OTHER INFORMATION: US-10-424-599-235443
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172689
LENGTH: 503
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 235443
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Matches
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 235443, Application US Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                     TITLE OF INVENTION: Soy Nucleic Acid TITLE OF INVENTION: Plants and Uses FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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ORGANISM: Oryza sativa
                                                                                                         TYPE: PRT
ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 VDGTIVAPSEPATWPANNKRNWLVFYRADGVSLVGAGLIDGKGQKWWDLPCKPHKGGNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 IFGSLEASSKISDY--KDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 VKDFGAAGDGVTDDTDALKTAWDTACADDGAGVVLAAAGRSFLIHTTVFTGPCQGSVTLQ 173
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   728;
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Thereof for Plant Improvement
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     DB 12;
1.3e-60;
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APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 44707

LENGTH: 456

TYPE: no.
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US-10-425-114-44707
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Best Local S
Matches 158
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Publication No. US20040034888A1
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                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: 700847226_FLI.pep-10-425-114-44707
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                   179 MLESNGRLP-STKPTALRFYGSDGVTVTGITIQNSQQTHLKFDSCTNVQVSGISVSSPGD
                                                                                                         119 FQLDGKIIAPTSSEAWGSGTLQWLEFSKLNTITIRGKGVIDGQGSVWWNNDSPTYNPTEV 178
                                                                                                                                          136 VKIFGSLEASSKISDYKDRRL-WIAFDSVQNLVVGGGGTINGNGQVWW------PSSC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399
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SPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGN
                                                                    KI--NKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAK 244
                                                                                                                                                                             NVLDYGAKGDGHADDTKAFEDAWAAACKVEGST-MVVPSGSVFLVKPISFSGPNCEPNIV
                                                                                                                                                                                                                 NVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGP-CRSSIS 135
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42.9%; Pred. No. 1.4e-60;
tive 51; Mismatches 139;
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US-10-362-091-4
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US-10-362-091-4
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Publication No. US20040049809A1
GEMERAL INFORMATION:
APPLICANT: Instituto de Cincia Aplicada e Tecnologia (ICAT)
TITLE OF INVENTION: Pear genes codifying for b-Galactosidase, Pectin Methylesterase,
TITLE OF INVENTION: Polygalacturonase, Expansin and their use.
FILE REFERENCE: none
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: PT 102511 C
PRIOR APPLICATION NUMBER: PT 102511 C
PRIOR FILING DATE: 2000-08-22
NUMBER OF SECTION OF THE PRIOR OF THE PRIOR FILING DATE: 2000-08-22
NUMBER OF SECTION NO. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
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Best Local Similarity
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TYPE: PRT
373
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                                                                                                                                                                                                                                                                                                                                                                                               81 AVFSGPCKNNAITFRIAGTLVAP---SDYRVIGNAGNWLLFQHVNGVTI-SGGVLDGQGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SITNVDAAAV-TFSVSSLGÄKADGSTDSTKAFLSÄWSNÄCASVNPAVIYVPAGR-FLLGN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                      ITFSGPCR-SSISVKIFGSLEASSKISDYK---DRRLWIAFDSVQNLVVGGGGTINGNGQ 179
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                                                                                                                                                           LGKDQQEAGVQNVTVKTVTFTGTENGVRIKSWGRPSTGFARSILFQHIVMTNVQNPIVID
                                                                                                                                                                                                                                                                           NASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGS 299
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                                     SGKPSEATCKNVHFNNAEHVTP
                                                                                                               QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                                                                LGSGNSEAYVSNVTVNEAKIIGAENGVRIKTW-QGGSGQASNIKFLNVEMQDVKYPIIID 358
                                                                                                                                                                                                                                        NAAGNSPNTDGIHVQMSSGVTILDSKISTGDDCVSVGPGTTNLWIENVACGPGHGISIGS
                                                                                                                                                                                                                                                                                                                    GLW--DCK-SSGKSCPSGATTLSFSNSNNVVVSGLISLNSQMFHIVVNGCQNVKMQGVKV 193
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                                                                            QNYCPNDKGCPGQASGVKVSDVTYQDIHGTSATEVAVKFDCSSMYPCNGIRLQDVKLT-Y 372
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; Sequence 284649, Application

US/10424599

RESULT 14 US-10-424-599-284649

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US-10-437-963-155040

Sequence 155040, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules I
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILLNG DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 284649
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 155040
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Best Local Similarity
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                                      APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US20040031072A1
                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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APPLICANT: Kovalic David K
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                                                                                                                                                                                                         Zhou, III.
                                                                                                                                                                                                                                Kovalic, par.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVKIFGSLEASSKISDYKD----RRLWIAFDSVQNLVVGGGGGTINGNGQVWWPSSCKINK- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KE-CLNQTSAVHVNDVSYSNIKGTYDVRTAPIHFACSDTVACTNITLSEVELLPFEGALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEDVRSFGAVGDGCADDTRAFRAAWKAACAVDSGI-VLAPENYSFKITSTIFSGPCKPGL
                                                                                                                                                                                                     Cao, You
Wu, Wei
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                                                                                                                                                             Barbazuk, Brad
                                                                                                                                                                           Boukharov, Andrey A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza
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 377
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                                                                                                                                                                                                                                                                                                                                                                                132 SS-ISVKIFGSLEA-SSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKIN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148;
                                                                                                                                                                                                                                                                                                          190 KSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                72 GIKVINVLSFGAKGDGKTYDNIAFEQAMNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR 131
                                 KPSEATCKN 429
                                                                                                                                                                      SNYTVNEAKIIGAENGVRIKTWQGGSGQAS-----NIKFLNVEMQDVKYPIIIDQNYC
                                                                                                                                                                                                         GIHVQSSSAVTITGASIQTGDDCISVGPGTSNLRVEHVSCGPGHGISIGSLGKESEEGGV
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                                                                   PNDGGQGCPHQSSDVQISGVTYTDIQGSSASQVAVKFDCSASKPCSGLGLQDIKLTFDGG
                                                                                                                                       ENVIVSGAAFVGTENGLRIKTW----GRAARSGAYVRGVVFEHALMRDVSNPIIIDQSYC
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KPAEATCQH
                                                                                                  --DRVBPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESG
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Pred. No. 3.9e-58;
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Search completed: July 21, 2004, 17:17:48 Job time: 82.2655 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2390
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	6	υ	4	(J)	2	<b>1</b>	Result
	702.5	704	704	704.5	708.5	710.5	711.5	715	718	718.5	727	728	736	741.5	749.5	764	787	787.5	787.5	796.5	840.5	898.5	1091	1108	1115.5	1127	1128	1142	2390	Score
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,	hypothetical prote	polygalacturonase	probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	$^{\circ}$	probable polygalac	polygalacturonase-	probable polygalac		probable polygalac	lac	probable polygalac	ein	Jun a 2 protein -	12		probable polygalac	a	probable polygalac	hypothetical prote	polygalacturonase		probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	polygalacturonase	ı

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	ب 4	33	32	31	30
659	662.5	667	673	673.5	678.5	680.5	683	684	687	687.5	688.5	690	696	698.5	701.5
27.6	27.7	27.9	28.2	28.2	28.4	28.5	28.6	28.6	28.7	28.8	28.8	28.9	29.1	29.2	29.4
414	664	407	444	387	445	394	394	397	383	393	492	540	384	452	542
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E85204	A84742	S52006	S34200	T07591	S34266	T00668	F86190	F96680	T47809	S40123	C96521	B96631	E84871	C85024	Н86239
polygalacturonase-	probable polygalac	polygalacturonase	polygalacturonase	polygalacturonase	polygalacturonase	probable polygalac	hypothetical prote	F5I14.10 [imported	polygalacturonase-	polygalacturonase	protein F21D18.18	probable polygalac	probable polygalac	probable polygalac	protein F20B24.8 [

## ALIGNMENTS

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RESULT 2
S31195
S31195
C)Species: Persea americana (avocado)
C)Species: Persea americana (avocado)
C)Species: Persea americana (avocado)
C)Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S31195; S28072
R,Dopico, B.; Lowe, A.L.; Wilson, I.D.; Merodio, C.; Grierson, D.
R,Popico, B.; Lowe, A.L.; Wilson, I.D.; Merodio, C.; Grierson, D.
R,Pittle: Cloning and characterization of avocado fruit mRNAs and their expression A;Reference number: S31195
A;Accession: S31195
A;Accession: S31195
A;Accession: S31195
A;Accession: S31195
A;Rocession: S31195
A;R
                                                                                                                                                                                                                     submitted to the EMBL Data Library, May 1992
A;Reference number: $28072
A;Accession: $28072
A;Molecule type: mRNA
A;Residues: 1-181 'S',183-462 <DO2>
A;Residues: 1-181 'S',183-462 <DO2>
A;Cross-references: EMBL:X66426; NID:g22630; PIDN:CAA47055.1; PID:g22631
C;Superfamily: polygalacturonase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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F;26-71/Domain: propeptide #status predicted <PRO>
F;72-444/Product: polygalacturonase 2A #status experim
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100.0%; Pred.
                                                                                                                       Score 1142; DB 1;
Pred. No. 2.6e-73;
7; Mismatches 106;
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.. No. 9.6e-162;
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C;Species: Cucumis melo (muskmelon)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-May-2000
C;Accession: T08215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: polygalacturonase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-461/Product: polygalacturonase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Hadfield, K.A.; Rose, J.K.; Yaver, D.S.; plant Physiol. 117, 363-373, 1998
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A; Residues: 1-461 < HAD>
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SGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNY
                                                                                                                       SAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLG 301
                                                                                                                                                                                                                               WPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
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                                                                                                                                                                                                                                                                                                                                                                                    EKMVSSPLASPEIFNVDDYGAMGDGED-DTEAFKETWKDACSSTNAI-FLVPCDRVYHLK 132
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                                                                              PGNSPNTDGIHVTGTQFIVIKNCLIMTGDDCISIVSGSKNVRAKGITCGPGHGISIGSLG
                                                                                                                                                                                 WLNSCKVNKTLPCKEAPTAVTFYQCTNLRVEGLRFRNAQQMLLSFQRCNNVKALNLWIYA
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Pred. No. 2.5e-72;
9; Mismatches 129;
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A;Reference number: Z23014
A;Reference number: Z23014
A;Accession: T46187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-431 <BEN>
A;Residues: 1-431 <BEN>
A;Cross-references: EMBL:AL133248; PIDN:CAB66108.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polygalacturonase (EC 3.2.1.15) precursor (similari N;Alternate names: protein T8H10.110 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 C;Accession: T46187; T50674 R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 85/3; 129/3; 186/3; 193/3; 263/1; 290/2; 326/3; 364/3
A;Introns: 85/3; 129/3; 186/3; 193/3; 263/1; 290/2; 326/3; 364/3
C;Superfamily: polygalacturonase
C;Keywords: glycosidase, hydrolase
C;Keywords: glycosidase, hydrolase
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-431/Product: polygalacturonase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z25172
A;Accession: T50674
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-431 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: cultivar Columbia; BAC R;Jenkins, E.S.; Roberts, J.A. submitted to the EMBL Data Library, December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewo
submitted to the Protein Sequence Database, January 2000
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T46187
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A;Experimental source: cultivar Landsberg erecta
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                                GISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKY
                                                                                VSNVEITAPGDSPNTDGIHITNTQNIRVSNSDIGTGDDCISIEDGTQNLQIFDLTCGPGH
                                                                                                                     ASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGH
                                                                                                                                                                                       INGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                                                                                                                                                                                                                                  GKTYLLKSTRFRGPCKSLRNFQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                                                                                                                                                                                                                            NKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
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  GISIGSLGDDNSKAYVSGINVDGAKFSESDNGVRIKTYQGGSGTAKNIKFQNIRMENVKN
                                                                                                                                                                   INGNGKTWWQNSCKIDKSKPCTKAPTALTLYNLKNLNVKNLRVKNAQQIQISIEKCNKVE
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                                                                                                                                                                                                                                                                                                                                                                                                                        AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL-----SLISSD
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                                                                                                                                                                                                                                                                                                                                     ----TVSVSNFGAKGDGKTDDTQAFKKAWKKACSTNGVTTFLVPK
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Pred. No. 2.7e-
71; Mismatches
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A;Gene: At2g41850
A;Map position: 2
C;Superfamily: poi
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable polygalacturonase [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_charc;Accession: H84846
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C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-426 <STO>
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222; Conserv
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                                                                                                                     QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE 418
                                                                                                                                                                                                        SLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIID
                                                                                                                                                                                                                                                VTAPADSPNTDGIHITNTQNIRVSESIIGTGDDCISIESGSQNVQINDITCGPGHGISIG
                                                                                                                                                                                                                                                                                       INASAKSPNTDGVHVSNTQXIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIG
                                                                                                                                                                                                                                                                                                                                   ETWWQNSCKRNKA-----KALTFYNSKSLIVKNLKVRNAQQIQISIEKCSNVQVSNVV
                                                                                                                                                                                                                                                                                                                                                                            QVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLM
                                                                                                                                                                                                                                                                                                                                                                                                                      LKSIQLTGPCNSILTVQIFGTLSASQKRSDYKDISKWIMFDGVNNLSVDGGDTGVVDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG---GTINGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLVTVFLLWALLMFSWCKASRISPNVYDHSYKRFKSDSLIKRR--EDITGLRSFVRASLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIKG----GTASCKNANVKNOGTVSPKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLVGESGKPSEATCKNVHFNNAEHVTPHCT
                                     SGKPSEATCKNVHFNNAEHVTPHCTS
                                                                              QDYCDK-SKCTTEKSAVQVKNVVYRDISGTSASENAITFNCSKNYPCQGIVLDRVNIKG-
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-GKATCTŇANVVDKGAVLPQČNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.7%;
49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TVSVSDFGAKGDGKTDDTQAFVNAWKKACSSNGAVNLLVPKGNTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1115.5; DB 2;
Pred. No. 1.7e-71;
4; Mismatches 117;
425
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lon, L
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RESULT S71523

polygalacturonase
N;Alternate names:

(EC

3.2.1.15)

[similarity]

peach

endopolygalacturonase

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A;Note: this is a revision to the sequence from reference S71: R;Lester, D.R.; Speirs, J.; Orr, G.; Brady, C.J. submitted to the EMBL Data Library, January 1994
A;Description: Homologies to the tomato endopolygalacturonase A;Reference number: S71524
A;Accession: S71524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X77231
A;Experimental source: cultivar Maravilla
A;Experimental source: cultivar Maravilla
A;Note: this sequence has been revised in reference S715
A;Lester, D.R.; Speirs, J.; Orr, G.; Brady, C.J.
Plant Cell Env. 13, 513-521, 1990
A;Title: Homologies to the tomato endopolygalacturonase
A;Reference number: S71525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 53-92, 'I', 94-149, 'T', 151-185, 'W', 187-196, 'THA', 200, 'ESLS', 206-207, 'TNT', 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lee, E., Speirs, J.; Gray, J.; Brady, C.J.
submitted to the EMBL Data Library, April 1994
A;Description: Homologies to the tomato endopolygalacturonase
A;Reference number: S71523
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A; Residues: 265-458 < LEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S71525
A;Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X77231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X77231; NID:g479087; PIDN:CAA54448.1; PID:g479088
A;Experimental source: cultivar Maravilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
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Best Local :
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Keywords: glycosidase; hydrola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues: 1-458 <LEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Prunus persica (peach)
Date: 19-Mar-1997 #sequence revision 19-Mar-1997
Accession: $71523; $71524; $71525
                                        402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVIQRNSILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLS----
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                                      NFPCEGIIMENINIVGESGKPSEATCKNVHFNNAEHVTPHCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                SSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSV
SVPCQGIVLQNIQL ---
                                                                                                                 FLNVEMQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYBNIKGTSATKVAIKFDCST
                                                                                                                                                                QATDITCGPGHGISIGSLGEDNANDHVSGVFVNGAKISGTSNGVRIKTWQGGSGSASNIV
                                                                                                                                                                                                    QATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIK
                                                                                                                                                                                                                                                 HVRFQNCKNVEASHLTVTAPEDSPNTDGIHITNTKNITISSSVIGTGDDCISIVSGSQRV
                                                                                                                                                                                                                                                                                      HIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNV
                                                                                                                                                                                                                                                                                                                                                                   QNLVVGGGGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNLKSKNAQQI
                                                                                                                                                                                                                                                                                                                                                                                                                SSNGAIVLVVPQ-KTYLVRPIEFSGPCKSHLTMQIYGTIEASDDRSVYKDVTHWLIFDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKFMEFIKPRAOLFSSRKLERAGSKSSSSVKTISVANFGAKGNGAD-DTRAFEKAWKAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MALQKHLVLFYVVVSFCAASCYSSGFQEVNSLHSFVDH--EKESGYNSRAHPSNMNTIEG
                                                                               FQNVEMNDVTNPIIIDQNYCDHKNKDCTRQRSAVQVKNVLYQNIRGTSASTDAITFNCSQ
                                                                                                                                                                                                                                                                                                                            QSLLVVGPGTINGNGNRWWENSCKRKPQPPCNEQAPTAVTFNKCNNLVVKNLKIQDAQQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.4%; Score 1108; I
48.9%; Pred. No. 6.56
tive 82; Mismatches
-QNARAKCNNVKPAYKGAVSPRCS
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6.5e-71;
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C;Accession: D96833
R;Theologis, A.; Ecker, J.R.; Palm, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Cc
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,

Liu,

Johnson-Hopson, C.; S.X.; Liu, Z.A.; Lui

C.; Khan, S.; Luros, J.S.;

Khaykin, E.; Kim, C. Maiti, R.; Marziali,

J.,

C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;

0. Dewar, Alonso, ewar, K.; #text\_change 23-Mar-2001

RESULT D96833

hypothetical protein F18B13.25 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change

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polygalacturonase (EC 3.2.1.15) - apple tree
N;Alternate names: poly [1,4-a-D-galacturonide] glycan hydrolase
C;Species: Malus domestica (apple tree)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T17011
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C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-460 < ATK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A cDNA clone for endopolygalacturonase from apple A;Reference number: Z18649; MUID:95062722; PMID:7972500 A;Accession: T17011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Pathway: polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Description: catalyzes hydrolysis of 1,4-alpha-D-galactosiduronic linkages in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                           IVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGG 334
                                                                                                                                                                                                                                                                                 NIQDAQQIHVIFQNCINVQASCLTVTAPEDSPNTDGIHVTNTQNITISSSVIGTGDDCIS
                                                                                                                                                                                                                                                                                                                                                                                                                        LWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIEGLKVMELIRPRTQLFSSRKLNTI-TGGIATSSAPAKTISVDDFGAKGNGAD-DTQAF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALKTQLLWSFVVVFVVSFSTTSCSGSSFQEVNALHSYVDHVDDKESGYNSRAYPSY-TD 59
ATTLNCSQSVPCQGTVLQSVQL--QNGR---AECNNVQPAYKGVVSPRC 460
                                       AIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHC 442
                                                                                        SGSATNIVFQNVQMNDVTNPIIIDQNYCDHKTKDCKQQKSAVQVKNVLYQNIRGTSASGD 416
                                                                                                                                  SGQASNIKFLNVEMQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYENIKGTSATKV 393
                                                                                                                                                                                   IVSGSQRVQATDITCGPGHGISIGSLGEDGSEDHVSGVFVNGAKLSGTSNGLRIKTWKGG
                                                                                                                                                                                                                                                                                                                             KSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCIS 274
                                                                                                                                                                                                                                                                                                                                                                            HWLIFDNVQNLLVVGPGTINGNGNIWWKNSCKIKPQPPCGTYAPTAVTFNRCNNLVVKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKAWKAACSSSGAMVLVVPQ-KNYLVRPIEFSGPCKSQLTLQIYGTIEASEDRSIYKDID 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WVIQRNSILLLIIIFASSIST--CRSNVIDD-NLFKQVYDNILEQEFAHDFQAYLSYLSK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1091; DB 2;
Pred. No. 1.1e-69;
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D9683 A;Status: preliminary A;Status: preliminary A;Rolecule type: DNA A;Residues: 1-459 <2500> A;Cross-references: GB:AE005173; NID:g5902387; PIDN:AAD55489.1; GSpDR.CMCC;Genetics: A;Gene: F18B13.25 A;Map position: 1 C;Superfamil:
probable polygalacturonase F24J13.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-20 C;Accession: H9672B R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Whi Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khayk C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Su ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Rocession: H96728
A;Residues: 1-468 <5TO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCANQLNIEPEKLSKTQKLQTSAISIENISFVHVRGTSASKEAIKISCSDSSPCRNILLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEVRDITVDTAIISDTANGVRIKTWQGGSGLVSKIIFRNIKWNNVSNPIIIDQYYCDSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNYCDRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGPGHGISIGSLGSGNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINKSLPCRDAPTALITWNCKNLKVNNLKSKNAQQIHIKFESCINVVASNLMINASAKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCKARLTLQISGTIIAPNDPDVWEGLNRRKWLYFHGLSRLTVEGGGTVNGMGQEWWERSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCRSSISVKIFGSLEASS--KISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSC
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Pred. No. 4.6e-56;
2; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIME
                                                                                                                                                                                                                                                                                            C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
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                                                                                                                                                             A.M.;
                                                                                                                                                                                                       Khaykin, E.; Kim, C
Maiti, R.; Marziali
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A;Cross-references: G
C;Genetics:
C;Gene: F24Ul3.7
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                   146
440 DDKSL
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                                                                                                                                                                                                                                                                                                                                       RRIWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNN
                                                                                                                                                                                                                    SIVSGSQNVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQG
                                                                                                                                                                                                                                                                                                                                                                                                              EQAMNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKIS--DYKD
                                                            AINFKCSDAVPCSHIVLNNINLEGNDGK-VEAYC--
                                                                                          AIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEH-----VTPHCTSLEIS
                                                                                                                         GNGYVKGVRFENVVMQDVANPIIIDQFYCDSPSTCQNQTSAVHISEIMYRNITGTTKSSK
                                                                                                                                                         GSGQASNIKFLNVEMODVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKV
                                                                                                                                                                                        SIVNGSAKIKMKRIYCGPGHGISIGSLGQGHSKGTVTAVVLETAFLKNTTNGLRIKTWQG
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                                                                                                                                                                                                                                                                                  LKSKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNILEQEFAHDFQAYLS-YLSKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
444
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41.6%;
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Pred.
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                                                              -NSAEGFGYGVVHPSADCLYSH
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polygalacturonase Cha o 2 - Japanese cypress
C;Species: Chamaccypris obtusa (Japanese cypress)
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_ch
C;Accession: JC7100; PC7026
R;Mori, T:; Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.
Biochem. Biophys. Res. Commun. 263, 166-171, 1999
A;Title: Purification, identification, and cDNA cloning of (A;Reference number: JC7100; MUID:99417540; PMID:10486272
A;Accession: JC7100
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A;Accession: JC7100
A;Accession: JC7100 Вb Ş Вb Š A; Molecule type: protein A; Residues: 51-62 < MO2> S A; Accession: PC7026 Matches Query Match Local 48 12 œ Similarity TFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS V---DKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67 LVHSRHDAATVFNVEQYGAVGDGKHDSTEAFATTWNAACKKASAV-LLVPANKKFFVNNL Conservative 33.3%; 73; Score 796.5; DB Pred. No. 9e-49; 3; Mismatches 1 DB 168; 2; #text\_change Length 514; Indels of × Cha 0 31; 11-May-2000 2, RSNRSLKK the second 47 major

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A;Cross-references: GB:
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Mait
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Saliberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,:fittle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Map position: 1
C;Superfamily: po
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A;Accession: A96609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                            LVPYTFCFLVKPTTFNGPCRTNLVLQIDGFIVSPDGPRSWPSNY--QRQWNMFYRVNGLS
                                         NVQATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASN
                                                                             QFHVRFDNCSDVVVDSVIIKAPASSPNTDGIHIENTHNVQIRNSMISNGDDCISIGAGCF
                                                                                                                                                    IQGSGVINGRGQKWWNLPCKPHKGLNGTTQTGPC-DSPVAIRLFQSSKVRIQGINFWNSA
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       NVDIKNVTCGPSHGISIGSLGVHNSQAYVSNITVTNSTIWNSDNGVRIKTWQGGSGSVSR
                                                                                                                                                                                                                                                                                                  YLSPSPAPNPAYNDNDNIAPTVFDVTSFGAIGDCSTDDTSAFKMAWDAACMSTGPKSALL
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                                                                                                                                                                                                                                                                                                                                                                         Score 787.5; DB 2;
Pred. No. 3.1e-48;
SB; Mismatches 155;
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.S.; Maiti, R.;
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second major allergen Cry j II precursor - Japanese cedar (,Species: Cryptomeria japonica (Japanese cedar) C,Species: Cryptomeria japonica (Japanese cedar) C;Date: 16-Mar-1995 #sequence revision 26-May-1995 #text_change 21-Jul-2000 C,Accession: JC2498; PC2346, Ā60147 R,Komiyama, N.; Sone, T.; Shimizu, K.; Morikubo, K.; Kino, K. Biochem. Biophys. Res. Commun. 201, 1021-1028, 1994 A,Title: CDNA cloning and expression of Cry j II, the second major allergen A,Reference number: JC2498; MUID:94271186; PMID:8002972
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RESULT 12
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A;Residues: 1-514 <NAM>
A;Cross-references: GB:D37765; NID:g577695; PIDN:BAA07021.1; PID:d1007598; PID:g577696
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                                                                                                                                                                                                                                                                                      CDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGK 421
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                                                                                                                                                                                         CTSASACQNORSAVOIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSGK
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; Pred. No. 3.9e-48;
78; Mismatches 163
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Biochem. Biophys. Res. Commun. 275, 195...
Biochem. Biophys. Res. Commun. 275, 195...
A;Title: Purification, identification, and A;Reference number: JC7366
A;Accession: JC7366
A;Molecule type: mRNA
A;Residues: 1-507 <YOK-
A;Cross-references: GB:AJ404653
A;Accession: PC7093
A;Molecule type: protein
A;Residues: 55-63 <YO2-
C;Comment: This protein, a second major of the polygalacturonase family.
C;Keywords: glycoprotein; pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui Allergy 45, 309-312, 1990
A;Title: Identification of the second major allergen of A;Reference number: A60147; MUID:90342988; PMID:2382797
A;Accession: A60147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1-54/Domain: signal sequence #status predicted F;55-460/Product: second major allergen Cry j #st F;429,460,472/Binding site: carbohydrate (Asn) (\alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 55-64 < SAK>
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A;Molecule type: mRNA
A;Residues: 1-514 <KOM>
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A; Residues: 52-61 < KO2>
                                                                                                                                                                                                                                                               C;Species: Juniperus ashei (mountain cedar)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_char
C;Accession: JC7366; PC7093
R;Yokoyama, M.; Miyahara, M.; Shimizu, K.; Kino, K.; Tsunoo,
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Best Local Similarity
Matches 168; Conserv
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Pred. No. 4.2e-48;
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and cDNA
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C;Genetics:
A;Gene: F280
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: B86368
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A; Residues: 1-1161 <STO>
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                                                                                                                                                             71 NGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPC 130
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Pred. No. 5.8e-45;
3; Mismatches 133;
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Search completed: July 21, 2004, 17:08:51 Job time: 34.3576 secs

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial	galactostopicultillians of the galactorions of the galactorions.  -!- SUBCELLULIAN LOCATION: Secreted!- BLOTECHNOLOGY: The effect of PG can be neutralized by introducing an antisense PG gene by genetic manipulation. The Plavr Savr tomato produced by Calgene (Monsanto) in such a manner has a longer shelf life due to delayed ripening!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.	[4]  REVISIONS.  Hiatt W.R.;  Submitted (OCT-1987) to the EMBL/GenBank/DDBJ databases.  Submitted (OCT-1987) to the EMBL/GenBank/DDBJ databases.  -I- FUNCTION: Acts in concert with the pectinesterase, in the ripening process. Is involved in cell wall metabolism, specifically in polyuronide degradation.  -I- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  -I- GATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  -I- GATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  -I- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-	[3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Sheehy R.E., Pearson J., Brady C.J., Hiatt W.R.; "Molecular characterization of tomato fruit polygalacturonase."; mol. Gen. Genet. 208:30-36(1987).	SEQUENCE FROM N.A. STRAIN=cv. Ailsa Craig; STRAIN=cv. Ailsa Craig; MEDLINE=87066731; PubMed=3786135; MEDLINE=87066731; PubMed=3786135; MEDLINE=87066731; PubMed=3786135; MEDLINE=87066731; PubMed=3786135; MEDLINE=87066731; PubMed=3786135; MEDLINE=87066731; PubMed=3786731; Ray J., Bird C.R., Schuch W.; Michael C.R., Schuch W.; Michael M., Schuch	(1) SEQUENCE FROM N.A. STRAIN-CV. Ailsa Craig; Bird C.R., Smith C.J.S., Ray J.A., Moureau P., Bevan M.W., Bird C.R., Smith C.J.S., Morris P.C., Grierson D., Schuch W.; "The tomato polygalacturonase gene and ripening-specific expression in transgenic plants."; plant Mol. Biol. 11:651-662 (1988).	LYCES LYCES STANDARD; PRT; 457 AA.  PGIR LYCES STANDARD; PRT; 457 AA.  POSLT7; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) Polygalacturonase 2A precursor (EC 3.2.1.15) (PG-2A) (Pectinase). Lycopersicon esculentum (Tomato). Lycopersicon esculentum (Tomato). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Lamiids; Solanales; Solanaceae; Solanum.  NCBI_TaxID-4081;

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ACT SITE
CARBOHYD
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SEQUENCE
  Polygalacturonase precursor Actinidia chinensis (Kiwi)
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InterPro; IPR006626; PbH1.
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# an email to license@isb-sib.ch)
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precursor (EC 3.2.1.15) (PG
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EMBL; L12019; ASC14453.1; -.

InterPro; IPRO00743; Glyco hydro 28; 1.

Pfam; PF00295; Glyco hydro 28; 1.

PROSITE; PS00502; POLYGALACTURONASE;

PROSITE; PS00502; POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Plant Physiol. 103:669-670(1993).
-!- FUNCTION: Acts in concert with the pectinesterase, in the ripolycenses. Is involved in cell wall metabolism, specifically in polyuronide degradation.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.
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MEDLINE=94302157; PubMed=8029342;
Atkinson R.G., Gardner R.C.;
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N-SA9A61483C028B7A CRC64;
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Pred. No. 1.1e
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01-JUL-1993
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                                                                                                                                        CARBOHYD
CONFLICT
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ACT_SITE
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Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopn
Eukaryota; Madmoliophyta; magnoliids; Laurales; Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Ripening-related polygalacturonase cDNA from avocado."
Plant Physiol. 103:289-290(1993).
-!- FUNCTION: Acts in concert with the pectinesterase,
process. Is involved in cell wall metabolism, speci
polyuronide degradation.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-
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STRAIN=cv. Hass; TISSUE=Pericarp;
MEDLINE=93184201; PubMed=8095163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
10-UCT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Hass; TISSUE=Mesocarp;
MEDLINE=94269193; PubMed=8208850;
Kutsunai, S.Y., Lin A.C., Percival F.W., Laties G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dopico B., Lowe A.L., Wilson I.D., Merodio C., Grierson D.; "Cloning and characterization of avocado fruit mRNAs and their expression during ripening and low-temperature storage."; Plant Mol. Biol. 21:437-449(1993).
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00295; Glyco_hydro_28; SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L06094; AAA329; PIR; S31195; S31195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00502;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
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  Local Sir hes 223;
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DEVELOPMENTAL STAGE: In ripening fruit.

SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
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POLYGALACTURONASE; 1.
POLYGALACTURONASE; 1.
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55.1%;
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    67;
  Pred. No. 1.70
7; Mismatches
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S -> I (IN REF. 2).
YIVG -> ILLE (IN REF.
LLREGLSTFLFMKRRVHECSY
                                          Score 1136;
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BY SIMILARITY.
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RESULT 4
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01-FEB-1996
10-OCT-2003
                                                                                                                                                                                                                                                                                              Atkinson R.G.;
"A cDNA clone for endopolygalacturonase from apple.";
Plant Physiol. 105:1437-1438(1994).
-!- FUNCTION: Acts in concert with the pectinesterase,
process. Is involved in cell wall metabolism, specipolyuronide degradation.
-!- CAFALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha.
galactosiduronic linkages in pectate and other gala-
-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
Malus domestica (Apple) (Walus sylvestris).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
           InterPro; IPR000743; Glyco_hydro_28.
Pfam; PF00295; Glyco_hydro_28; 1.
PROSITE; PS00502; POLYGALGTUROMASE;
Hydrolase; Glycosidase; Cell wall; S:
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=cv. Golden Delicious;
MEDLINE=95062722; PubMed=7972500;
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                                                                                 EMBL; L27743; AAA74452.1; PIR; T17011; T17011.
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                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to family 28 of glycosyl hydrolases
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              signal;
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                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                Fruit ripening;
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Best Local
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01-NOV-1995
01-NOV-1995
10-OCT-2003
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CHAIN
ACT SITE
CARBOHYD
CARBOHYD
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01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Possible polygalacturonase precursor (EC 3.2.1.15) (EC 4.2)
(Major pollen allergen Cry j 2) (Cry j II).
Cryptomeria japonica (Japanese cedar).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta;
Spermatcphyta; Coniferopsida; Coniferales; Cupressace, NCBI_TaxID=3369;
                                                                                                                                                                                                                                                                                                                                                 LT 5
CRYJA
             MEDLINE=94271186; PubMed=8002972; Komiyama N., Sone T., Shimizu K., "cDNA cloning and expression of C
                                                                                                              Namba M., Kurose M., Torigoe K.,
Usui M., Kurimoto M.;
"Molecular cloning of the second
 Japanese cedar pollen.";
                                                                SEQUENCE FROM N.A
                                                                                        Japanese cedar pollen."; FEBS Lett. 353:124-128(1994)
                                                                                                                                                     MEDLINE=95010777; PubMed=7926035;
                                                                                                                                                                 TISSUE=Pollen;
                                                                                                                                                                                SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSATNIVFQNVQMNDVTNPIIIDQNYCDHKTKDCKQQKSAVQVKNVLYQNIRGTSASGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVSGSQRVQATDITCGPGHGISIGSLGEDGSEDHVSGVFVNGAKLSGTSNGLRIKTWKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HWLIFDNVQNLLVVGPGTINGNGNIWWKNSCKIKPQPPCGTYAPTAVTFNRCNNLVVKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LWIAFDSVQNLVVGGGGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIEGLKVMELIRPRTQLFSSRKLNTI-TGGIATSSAPAKTISVDDFGAKGNGAD-DTQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALKTQLLWSFVVVFVVSFSTTSCSGSSFQEVNALHSYVDHVDDKESGYNSRAYPSY-TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVIQRNSILLLIIIFASSIST--CRSNVIDD-NLFKQVYDNILEQEFAHDFQAYLSYLSK
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                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 P(
460 P)
315 PI
280 N.
421 N-
49403 MW;
                                                                                                                                                                                AND PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%;
49.3%;
             Shimizu K., Mc
ression of Cry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE.

N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
13E99A7A049F4FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1091; DB 1;
Pred. No. 2.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYGALACTURONASE
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                 major allergen,
                                                                                                                                        Hino K.,
                          Morikubo K.,
              j II the
                                                                                                                                                                                                                                                                                                                                     514
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                                                                                                                                        Taniguchi Y., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                     Cupressaceae;
              C., Kino
                                                                                                                Cry
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                                                                                                                                                                                                                                                                        (PG)
              major
                          Ä
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                                                                                                                                                                                                                                 Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                 II,
                                                                                                                                                                                                                                                                        (Pectinase)
                                                                                                                                                                                                                     Cryptomeria
              allergen
                                                                                                                                                                                                                                                                                                                                                                                                                            442
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              of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
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Best Local :
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ACT_SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JC2498; JC2498.
PIR; S48730; S48730.
HSSP; P26509; 1BHE.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pollen.";
Allergy 45:309-312(1990).
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Amyloplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00502; POLYGALACTURONASE; 1.
Hydrolase; Glycosidase; Cell_wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000743; Glyco_hydro_28
InterPro; IPR006626; bbH1.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90342988; PubMed=2382797;
Sakaguchi M., Inouye S., Taniai M., Ando S.,
"Identification of the second major allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 55-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 201:1021-1028(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          galactosiduronic linkages in pectate and other galacturonans SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL). ALLERGEN: Causes an allergic reaction in human. SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                             107
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                                                                                                                                                              œ
                                                                                                                                                                                                 Similarity
                                                                                                                                                    TESGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPS 184
                                                                                                              VD----KNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQI
                                                                                                                                      VAMQLIIMAAA-----
QCKWVNGREICNDRDRPTÄIKFDFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITÄ
                    SCK-INKSLPC--RDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINA
                                           FFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGVIDGQGKQWWAG
                                                                                          VEHSRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAAC-KKPSAMLLVPGNKKFVVNNL
                                                                                                                                                                                                                                   514 AA;
                                                                                                                                                                                                                                                                                                                                                              23
46
434
278
460
472
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                             32.9%;
                                                                                                                                                                                                                                   56645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Allergen
                                                                                                                                                                                     78;
                                                                                                                                                                                                                                DI -> VV (IN REF. 2).
Q -> K (IN REF. 2).
K -> N (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 2).
K -> E (IN REF. 2).
G -> R (IN REF. 2).
M -> I (IN REF. 2).
M -> C (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
                                                                                                                                       -EDQSAQIMLDSDIEQ---
                                                                                                                                                                                                                                                                                                                                                                           PROBABLE.
N-LINKED
                                                                                                                                                                                                          Score 787.5;
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F -> L (IN REF.
V -> L (IN REF.
                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                 POSSIBLE POPENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .)
                                                                                                                                                                                                 .5e-48;
                                                                                                                                                                                                            ВB
                                                                                                                                                                                                                                                                                                                    163;
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of Japanese
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                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                           Length 514;
                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fruit
                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                       YL----RSNRSLRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ripening,
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                     241
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В
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                                                                                                                                                  RA Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Rhinite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Feng J.-D., Fong B., Fujii C.Y.,
RA Chung M.K., Conn L., Conway A.B., Fong J.-D., Fong B., Fujii C.Y.,
RA Chung M.K., Conn L., Conway A.B., Fong B., Fujii C.Y.,
RA Chung M.K., Coldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
Tequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase clone GBGE184 precursor (EC 3
(Pectinase) (Galacturan 1,4-alpha-galacturonidase)
PGA3 OR ATIGO2790 OR T14P4 2 OR F22D16.22.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Differential expression of a polygalacturonase Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99413295; PubMed=10485285; Torki M., Mandaron P., Thomas F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N. STRAIN=CV. C24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P49062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torki M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                         polygalacturonase.
CATALYTIC ACTIVITY
                                                                                              FUNCTION: May
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                                                                                                                 408:816-820(2000).
                  LYTIC ACTIVITY: {(1,4)-alpha-D-4)-alpha-D-galacturonide}(N-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEATCKNVHFNN--AEHVTPHCTSLEIS 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTSASACQNQRSAVQIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGSGMASHIIYENVEMINSENPILINQFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQDVKYPIIIDQNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAKSPNIDGVHVSNIQYIQISDIIIGIGDDCISIVSGSQNVQAINIICGPGHGISIGSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- TASCLNDNANGYFSGHVTPACKNLSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRDSPNTDGIDIFASKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGISIGSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Flower buds;
                                                                            germination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261:948-952(1999).
                                                                                            function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassicaceae;
                                                                            in depolymerizing p
on, and tube growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quigley F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
                  -galacturonide}(N)
+ D-galactur-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis
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              D-galacturonate
                                                                            g pectin
ch. Acts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mache R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                              as an
                                                                                            during
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                                                                                              pollen
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Best Local Similarity
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P48979;
01-FEB-1996
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ACT_SITE
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SEQUENCE
                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Polygalacturonase precursor (EC 3.2.1.
Prunus persica (Peach).
Eukaryota; Viridiplantae; Streptophyta
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                                                                                                                                                                                                            PRUPE
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SMART; SM00710; PbH1; 5.
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Multigene
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Y16230; CAA76127.1; -.
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Spermatophyta;

Magnoliophyta;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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1. FUNCTION: Acts in concert with the pectinesterase, in the ripprocess. Is involved in cell wall metabolism, specifically in polyuronide degradation.

2. CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.

3. UNICARITY: Belongs to family 28 of glycosyl hydrolases.
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Hydrolase; Glycosidase; Cell wall; Signal; Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P26509;
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"Peach (Prunus persica) endopolygalacturonase cDNA isolation and mRNA analysis in melting and nonmelting peach cultivars.";
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InterPro; IPR006626; PbH1.
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                              FSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGESGKPSEATCKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVASLGAKADGKTDSTKAFLSAWAKACASMNPGVIYVPAG-TFFLRDVVFSGPCKNNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITFSGPCR-SSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavorcrest;
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BY SIMILARITY
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 687.5;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53DCC26944D22BF9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 4.1e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Q39786;
15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, I
10-OCT-2003 (Rel. 42, I
                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
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ACT SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      galactosiduronic linkages in pectate and other galacturonic TISSUE SPECIFICITY: Pollen.
-:- TISSUE SPECIFICITY: Pollen.
-:- DEVELOPMENTAL STAGES, Appears 12 days before anthesis and levels are seen in pollen on the day of anthesis.
-:- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00295; Glyco hydro 28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U09717; AAA82167.1; PIR; S52006; S52006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA: tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic
                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cotton (Gossypium hirsutum L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Coker 312; TISSUE=Poll
MEDLINE=95161720; PubMed=7858233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                    Local L
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                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro; IPR006626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro; IPR000743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during pollination.

CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CATALYTIC accordances in pectate and other galact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Mol. Biol. 26:1989-1993(1994).
FUNCTION: May function in the depolymeria its walls during pollen tube elongation,
                                                         80
                                                                                                                                                  67
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                PS00502;
CENREFRSK-LPVNIRFDFLTNALIQDITSKDSKLFHINVFACKNITLERLKIEAPDESP
                           KINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVVASNLMINASAKSP
                                                         EGPCKAPIEINVQGTIQAPADPSAFKDPN-WVRFYSVENFKMFGGGIFDGQGSIAYEKNT 138
                                                                                    SGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGGGTINGNGQVWWPSSC 186
                                                                                                                                                  KVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLLKQITF
                                                                                                                      KVQSDAFDV--VAKFGAKADGKTDLSKPFLDAWKEACASVTPSTVVIPKG-TYLLSKVNL
                                                                                                                                                                                                                                                                                                                                                                               Glycosidase; Cell
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                                                                                                                                                                                 Conservative
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ry function in the depolymerization of the common of the common or in that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                um hirsutum L.) pollen-specific polygalacturonase
temporal specificity of its promoter in transgen
                                                                                                                                                                                                                                                                                                                                                                                                POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor
                                                                                                                                                                                                                                             43921
                                                                                                                                                                            27.9%; Score 667; DB 1; 38.4%; Pred. No. 1.2e-39; tive 69; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                               Glyco_hydro
PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
cursor (EC 3.2.1.15) (PG)
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SEQUENCE FROM N.A.
STRAIN=CV. C24; TISSUE=Flower buds;
MEDLINE=99413295; PubMed=10485285;
MEDLINE=99413295, PubMed=10485285;
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01-FEB-1996 (Rel. 33, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exopolygalacturonase clone GBGA483 precursor
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                                                                   Kiyokawa C., Kohara M., Matsumoto M., Matsuno Nakayama S., Nakazaki N., Shinpo S., Takeuchi Watanaba A., Yamada M., Tabata S., "Sequence and analysis of chromosome 3 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differential expression of a polygalacturonase Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pectinase) (Galacturan 1,4-alpha-galacturonidase)
AT3G07850 OR F17A17.19.
                                     "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21016720; PubMed=11130713;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261:948-952(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quigley F., Mache R.,
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                                                                                                                                          A., Muraki A
C., Wada T.,
                                                                          plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family
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Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
A Southwick A.M., WH H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
A Arakawa T., Banh J., Banno F., Bowser I., Brooks S.Y., Carninci P.,
A Arakawa T., Banh J., Banno F., Bowser I., Brooks S.Y., Carninci P.,
A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                     ACT_SITE
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X72292; CAA51033.1; ---
EMBL; X70219483; AAF21195.1; ---
EMBL; AV06173; AALO7022.1; ---
EMBL; AY091200; AAM14139.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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SEQUENCE FROM N.
STRAIN=CV. Colum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S34200; S34200.
InterPro; IPR000743; Glyco_hydro_28
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
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SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to family 28 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development, germination,
168 VGGGGTI-NGNGQVWWPSS-CKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIK
                                                                                                                                                                                                                                                      151;
                                                                                                                    42
                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                                                       Similarity
                                                  TI--TVPKGE-YMVESLEFKGPCKGPVTLELNGNFKAPATVKTTKPHAGWIDFENIADFT
                                                                                 PVQFVVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLV
                                                                                                                                                                                                                     ILLLIIIFASSISTCRSNVIDDNLFKQVYDNILEQEFAHDFQAYLSYLSKNIESNNNIDK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement
                                                                                                                     TAKNAATAVGGAAASVGAKVSGAKPGAAVDVKASGAKGDSKTDDSAAFAAAWKEACAAGS
                                                                                                                                                                                      LLVLLVVMATTIAN-GTPVVDK---
                                                                                                                                                                                                                                                                                                                                                                                                                                        family.
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284
222
342
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222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell
                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                      ; 68
                                                                                                                                                                                                                                                                       Score 667; DB 1;
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                        S -> G (IN REF. 1).
; DF1D4C30FB1C3F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                        EXOPOLYGALACTURONASE CLONE GBGA483 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        wall; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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and tube growth.
                                                                                                                                                                                                                                                       Mismatches
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o K., Cheuk F
                                                                                                                                                                                                                                                                                     Length 444;
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as an exo-
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                                            ACT SITE
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15-JUL-1998
15-JUL-1998
10-OCT-2003
                 CARBOHYD
CARBOHYD
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                                                                       CHAIN
ACT_SI
                                                                                                                              PROSITE; PS00502; POLYGALACTURONASE; 1.
                                                                                                                                           Pfam; PF00295; Glyco_hydro_28; 1. SMART; SM00710; PbH1; 5.
                                                                                                                                                                     EMBL; U09805; AAA58322.1; -.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core everyoids II; Malvales; Malvaceae; Malvoideae; Gossypi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polygalacturonase G9.
                                                                                                                 Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95161720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium barbadense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            John M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGLR
                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restroy non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                 galactosiduronic linkages in pectate and other galacturo
TISSUE SPECIFICITY: Pollen (By similarity).
SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: May function in the depolymerization of the pectin in its walls during pollen tube elongation, or in that of the pistil during pollination.

CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                       galactosiduronic linkages in TISSUE SPECIFICITY: Pollen (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Gossypium hirsutum L.)
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                                                                                                               Glycosidase;
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244
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and temporal specificity of its promoter in transgem
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42,
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42, Last annotation update)
precursor (EC 3.2.1.15) (PG)
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Gossypium.
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_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGLT MAIZE P35339;
                           the
                                                       This
                                                                                                                                                                                                    MEDLINE=93164262; PubMed=8433375; Barakate A., Martin W., Quigley F., Mach "Characterization of a multigene family exopolygalacturonase in maize ", J. Mol. Biol. 229:797-801(1993).
                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
10-CCT-2003 (Rel. 42, Last annotation
Exopolygalacturonase precursor (EC 3.2)
  modified
               use
                                         between
                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4577
                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                   Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                            (Galacturan 1,4-alpha-galacturonidase)
                         s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinformatics Institute.
                                                                              polygalacturonase.

(ATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N) + {(1,4)-alpha-D-galacturonide}.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Pollen.

DEVELOPMENTAL STAGE: Late stages of pollen development.

SIMILARITY: Belongs to family 28 of glycosyl hydrolases
                                                                                                                                                                   olygalacturous -...
(ol. Biol. 229:797-801(1993).

FUNCTION: May function in depolymerizing pectin
function, and tube growth. Acts
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                                                                                                                                                                                                                                                                      Missouri 17;
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  this statement is not removed.
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                institutions
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                                                                                                                                                                                                                                                                    TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 666; DB
Pred. No. 1.4e
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBE842A77158CCF0 CRC64;
                                       ght. It is produced through a collaboration Bioinformatics and the EMBL outstation -
               as long
                                                                                                                                                                                                                                             Mache
                                                                              of pollen development. of glycosyl hydrolases.
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2.1.67)
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l.4e-39;
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Usage
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Best Local S
Matches 131
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01-MAR-1992
01-MAR-1992
10-OCT-2003
MEDLINE=93005658; PubMed=2152116;
Brown S.M., Crouch M.L.;
"Characterization of a gene family abundantly expressed organensis pollen that shows sequence similarity to polygalacturonase.";
                                                                                                                                                                                                                                                          OENOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
ACT SITE
CARBOHYD
                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase (EC 3.2.1.67) (ExoPG) (Pectinase)
1,4-alpha-galacturonidase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IFN...
InterPro; IFN006626; PbH1.
InterPro; IPR006626; PbH1.
InterPro; IPR006626; PbH2.
InterPro; IPR0006826; I.
SMART; SM00710; PbH1; 5.
SMART; SM00710; PbH1; 5.
SMART; SM00710; PolygalacturoNaSE; 1.
SM1; Signal; Glycoprotein;
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embry, Spermatophyta; Magnoliophyta; eudicotyledons; Myrtales; Onagraceae; Oenothera.
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                                                                                                                                                        Oenothera organensis (Evening primrose).
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                                                                                                                                                                                                                                                                                                                                  AVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINL--VGESGKPSEATCKN
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5; Mismatches 143;
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Matches 129
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                                                                                                     P26216;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exopolygalacturonase precursor (EC 3.2.1.67)
(Galacturan 1,4-alpha-galacturonidase).
PG1 AND PG2 AND PG3 AND PG6 AND PG14.
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-!- FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polygalacturonase.
-i- CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N) + H(2)0
-i- (1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate.
-i- TISSUE SPECIFICITY: Pollen tubes growing through the style du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00295; Glyco_hydro_28;
SMART; SM00710; PbH1; 4.
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-!- SIMILARITY: Belongs to family 28 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollination.
-!- DEVELOPMENTAL STAGE: Accumulates late
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                                                                                          Zea mays (Maize)
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FUNCTION: May function in
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IPR006626; PbH1.
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Spermatophyta; Magnoliophyta; Liliopsida; PACCAD clade; Panicoideae; Andropogoneae; NCBI\_TaxID=4577;

Viridiplantae;

Streptophyta; E /ta; Liliopsida;

Embryophyta;

Poaceae;

Tracheophyta;

Zea Poales;

SEQUENCE FROM N.A., STRAIN=cv. Missouri

AND 17;

SEQUENCE OF 23 TISSUE=Pollen;

23-37

MEDLINE=92032781;

PubMed=1932692;

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PIR; S25824; S25824.
PIR; S30064; S30064.
MaizeDB; 25864; -.
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"Sequence analysis of three members of the maize p
gene family expressed during pollen development.";

Plant Mol. Biol. 20:343-345(1992).
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ACT_S
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MEDILINE=94035141; PubMed=8106080;
Allen R.L., Lonsdale D.M.;
"Molecular characterization of one of the maize "Molecular characterization of one of the maize which are expressed during
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
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MEDLINE=93164262; PubMed=8433375;
Barakate A., Martin W., Quigley F., Mache R.;
"Characterization of a multigene family encoding
"Characterization of a multigene family encoding
expolygalaturonase in maize.";
   CARBOHYD
                                                                       CARBOHYD
                                                                                                                                                                                   SIGNAL
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SMART; SM00710; PbH1; 5.
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MEDLINE=93004490; PubMed=139
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                                                                                                                                                                                                                                                                                    PROSITE; PS00502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polygalacturonase.

CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N)

{(1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Pollen.

DEVELOPMENTAL STAGE: Late stages of pollen developmen

SIMILARITY: Belongs to family 28 of glycosyl hydrolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X57627; CAA40850.1; ALT X57628; CAA40851.1; ALT X57743; CAA40810.1; -... X57743; CAA40803.1; -... X55844; CAA4680.1; -... X65845; CAA4660.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4249.1; -... X62385; CAA4229.1; -... X62385; CAA4290.1; -... X6285; CAA4290.1; -... X6285
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Lonsdale D.M.;
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                                                                                                                                                                                                                       POLYGALACTURONASE; 1.
POLYGALACTURONASE; 1.
PARRE: Cell wall; Signal; Glycoprotein;
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EXOPOLYGALACTURONASE.
PROBABLE.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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MEDLINE=93164262; PubMed=8433375;
Barakate A., Marctin W., Quigley F., Mache R.;
"Characterization of a multigene family encoding exopolygalacturonase in maize.";
J. Mol. Biol. 229:797-801(1993).
-I- FUNCTION: May function in depolymerizing pect
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VARIANT
SEQUENCE
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01-JUN-1994
                                                                                                                                                                                                                                                                                                                  PACCAD clade; Panicoideae; Andropogoneae; NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIZE
PGLS_MAIZE
              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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10-OCT-2003
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                                                  polygalacturonase. {(1,4)-alpha-D-galacturonide}(N) + H(CATALYTIC ACTIVITY: {(1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate. {(1,4)-alpha-D-galacturonide}(N-1) + D-galacturonate. SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Pollen.

DEVELOPMENTAL STAGE: Late stages of pollen development. DEVELOPMENTAL STAGE: Late stages of glycosyl hydrolases. SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
                                                                                                                                                                  development, germination, and
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Best Local Sim:
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CARBOHYD
                                                                                                                                                              Q40312;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG
Medicago sativa (Alfalfa).
                                                                                                                                                                                                                                                                                                                                      MEDSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00295; Glyco_hydro_28; 1. SMART; SM00710; PbH1; 5.
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InterPro; IPR006626; PbH1.
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                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago
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PIR; S30066; 
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    STRAIN=CV.
                             SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=3879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                   STANDARD;
    TISSUE=Pollen;
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Pred. No. 8.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qiu X., Erickson L.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1995) to the depolymerization of the FUNCTION: May function in the depolymerization of the its walls during pollen tube elongation, or in that olduring pollination (By similarity).
-I- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacticity: Pollen specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 4.
PROSITE; PS00502; POLYGALACTURONASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U20431; AAA62286.1; --
PIR; T09398; T09398.
InterPro; IPR000743; Glyco_hydro_
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Glycosidase; Cell
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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    -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases

                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Match
361
                          410
                                                      306
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
LNNVDL-KFNGAPTTAKCTNV
                          MENINLYGESGKPSEATCKNV
                                                      VIIDQEYYPWNQCSKKNP----SKIKLSKISFKNVKGTSGTAEGVVLICSSAVPCDGVE
                                                                                 ILIDONA
                                                                                                             VGSLGKFTTEENVEGITVKNCTLTATDNGVRIKTWPDAPGTITVSDIHFEDITMTNVKNP
                                                                                                                                   IGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSG--QASNIKFLNVEMQDVKYP
                                                                                                                                                                  FTITAPGDSPNTDGIHMGKSTDVKILNTNIGTGDDCVSIGDGSKQITVQGVNCGPGHGLS
                                                                                                                                                                                          LMINASAKSENTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITCGEGHGIS
                                                                                                                                                                                                                                                     PCRDAPTALTFWNCKNLK-
                                                                                                                                                                                                                                                                            PIELQVDGTIQAPADPSVIKGTEQWFKFLYMDHLTLSGKGVFDGQGATVY
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                                                                                                                                                                                                                          PA-----SAWSGKNSNSKVFMNFGENFVNNSIVRGVTSKDSKNFHVMVFGCKNITFDG
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                           430
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           589.5;
No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 421;
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9: sp_phage:*

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11: sp_rodent:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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SEQUENCE FROM N.A.  TISSUE=Pericarp; MEDLINE=20252524; PubMed=10794531; MEDLINE=20252524; PubMed=10794531; Mang Z.Y., MacRae E.A., Wright M.A., Bolitho K.M., Ross G.S., Atkinson R.G.; Polygalacturonase gene expression in kiwifruit: relationship to fruit softening and ethylene production."; Plant Mol. Biol. 42:317-328 (2000):- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYGALACTURONASES). EMBL, AF152758; AAF71160.1; G0; G0:0005618; C:cell wall; IEA. G0; G0:0005618; C:cell wall; IEA. G0; G0:0004650; F:hydrolase activity, acting on glycosyl bonds; IEA. G0; G0:0004650; F:polygalacturonase activity; IEA. G0; G0:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR000743; Glyco hydro_28. InterPro; IPR000743; Glyco hydro_28. InterPro; IPR000626; PbH1. InterPro; IPR000626; PbH1. InterPro; IPR000626; PbH1. SMART; SM00710; PbH1. 4. SMART; SM00710; PbH1. 4. Cell wall; Glycosidase; Hydrolase. SEQUENCE 463 AA; 50352 MW; 7EED7EFE5498FA CRC64;	9M6S2 PRE 9M6S2; 1-OCT-2000 (Tx 1-OCT-2000 (Tx 1-UIN-2003 (Tx 0/1/201acturona GA. ctinidia chine ctinidia chine ukaryota; Viri permatophyta; ricales; Actin CBI_TaxID=36251

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GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bor
GO; GO:0016798; F:bydrolase activity; IEA.
GO; GO:0004650; F:polygalacturonase activity; IEA.
InterPro; IPR0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco hydro 28.
InterPro; IPR000626; RbH1.
InterPro; IPR000408; Reg_chr_condens.
Pf6am; PF00295; Glyco hydro 28; 1.
SWART; SW00710; PbH1; 4.
RPOSITE; PS00520; POLYGALACTURONASE; 1.
RPROSITE; PS00626; RCC1_2; 1.
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Best Local Similarity
Matches 256; Conserv
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
Polygalacturonase PG1.
                                                                                                                                                                                                                                          STRAIN=cv. Shiraz;
Nunan K.J., Davies C., Robinson S.P., Fincher G.B.;
"Characterization of cell wall modifying enzyme activ
corresponding cDNAs during grape berry development.";
                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO FAMILY 28 (POLYGALACTURONASES).
                                                                                                                                                                                                                                Planta
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29760;
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Query Match
Best Local Similarity
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Best Local (
                                                                                                    InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 6.
SMART; SM00710; PbH1; 6.
PROSITE; PS00502; POLYGALACTURONASE;
CC11 wall; Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                    EMBL; AF434714; AAL30418.1; --
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, actir
GO; GO:0016798; F:polygalacturonase activit
GO; GO:0004650; F:polygalacturonase activit
GO; GO:0005975; P:carbohydrate metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Williams 82; Christiansen L.C., Dal Degan F., Ulvskov P., Borkhardt E Christiansen L.C., Dal Degan F., ulvskov P., Borkhardt E "Examination of the dehiscence zone in soybean pods and dehiscence-related endopolygalacturonase gene."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLJ
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01-JUN-2003
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
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51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                         Score 1185.5;
Pred.
                                                                                  F553DBA6C297626D CRC64;
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No. 1.3e-69;
                                                                                                                                                                                                                                                                                                         activity;
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                                                                        EMBL; AC013483; AAF21207.1; -.

GO; GO:0005618; C:cell wall; IEA.

GO; GO:0016798; F:hydrolase activity, acting on

GO; GO:0016798; F:polygalacturonase activity; IE

GO; GO:0004659; F:carbohydrate metabolism; IEA.

InterPro; IPR000743; Glyco_hydro_28.

InterPro; IPR000408; Reg_chr_condens.

Pfam; PF00295; Glyco_hydro_28; 1.

SMART; SM00710; PbH1; 4.

PROCESSER SMART; SM00710; PbH1; 4.
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Q9SFB7;
01-MAY-2000
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Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F17A17 genomic
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2003 (TrEMBLrel. 24,
Putative polygalacturonase
                    PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1. Cell wall; Glycosidase; Hydrolase.
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  SEQUENCE
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0 (TrEMBLrel. 13,
3 (TrEMBLrel. 24,
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Query Match
Best Local Similarity
Matches 230; Conserv
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01-JUN-2002
01-JUN-2003
              EMBL; AY078936; AAL84942.1; -.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on
GO; GO:0004650; F:polygalacturonase activity; IE
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006743; Glyco_hydro_28.
InterPro; IPR006266; PbH1.
                                                                                                                                                                       "Arabidopsis cDNA clones.";
Submitted (FEB-2002) to the
-!- SIMILARITY: BELONGS TO I
                                                                                                                                                                                                                                                Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K. Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                       (POLYGALACTURONASES)
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FAMILY 28 OF GLYCOSYL HYDROLASES
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Last
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Pred. No. 1.4e
6; Mismatches
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Best Local Sim
Matches 226;
(POLYGALACTURONASES).

EMBL; AJ250919; CAC05658.1; -.

EMBL; AJ250918; CAC05657.1; -.

EMBL; AJ250918; CAC05657.1; -.

GO; GO:0005618; C:cell wall; IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl

GO; GO:0004650; F:polygalacturonase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                        Gonzalez-Carranza Z.H., Whitelaw C.A., Roberts J.A.; "Characterisation of a polygalacturonase gene (PGAZERAN) expressed during abscission in Brassica napus.", its relicion to senescence a comparison with its homologus gene in Arabidopsis thaliana (PGAZAT) submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                           Q9FDY7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Endopolygalacturonase.
                                                                                                                                                                                                                                             Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosideurosids II; Brassicales; Brassicaceae; Brassica.
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PROSITE; PS00626; RCCL 2; 1.
Cell wall, Glycosidase; Hydrolase.
Cell wall, Glycosidase; MW; 08E1EE62AA05A26B CRC64;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=3708;
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50.7%;
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Pred. No. 3
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Best Local 9
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InterPro; IPR006626; PbH1.
InterPro; IPR006408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE; 1
PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase.
SEQUENCE 434 AA; 46603 MW; E9249AC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998
01-NOV-1998
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cucumis melo (Muskmelon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Hadfield K.A., Rose
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46603 MW; E9249AC1BEC0C219
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Last annotation updat
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Pred. No. 5.6e-66;
8; Mismatches 117;
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          glycosyl bonds;
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Best Local S
Matches 224
           Submitted [2]
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01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update
Endo-polygalacturonase (At3g57510).
PGAI OR ADPGI OR T8H10.110 OR AT3G57510/T8H10_110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004650; F:polygalacturonase activity; I
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco hydro_28.
InterPro; IPR0006626; PbH1.
InterPro; IPR000408; Reg chr condens.
Pfam; PF00295; Glyco hydro_28; 1.
SMART; SM00710; PbH1; 4.
                                                                                                         Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryo
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PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase; Sign
SEQUENCE FROM N
                                   Sander L.,
Borkhardt
                                                                                              NCBI_TaxID=3702;
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                         STRAIN=cv.
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                                             E FROM N.A.
cv. COLOMBIA;
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                                                                                                                                                                                                                                                                                              DDKSAQAEASCKNVKWKNRGRVSPQC
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                        (OCT-1997)
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50.2%;
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                                               Ulvskov P.,
                      the
                                                                                                           Brassicaceae;
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                        EMBL/GenBank/DDBJ databases
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Pred. No. 8
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                                                Albrechtsen
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                                                                                                                    Embryophyta; Tracheophyta;
edons; core eudicots; rosids;
                                                                                                            Arabidopsis.
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                                               Joergensen
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Best Local
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GO; GO:0016798; F:hydrolase activity, ac
GO; GO:0004650; F:polygalacturonase act:
GO; GO:0005975; P:carbohydrate metaboli:
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR00626; PbHI.
InterPro; IPR00626; PbHI.
InterPro; IPR00408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbHI; 5.
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Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yenkins E.S., Roberts J.A.; "Dehiscence-related expression of an Arabidopsis thaliana gene "Dehiscence-related expression of an Arabidopsis thaliana gene encoding a polygalacturonase in transgenic plants of Brassica napus."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ002532; CAA05525.1;
EMBL; AF037367; AAC98923.1;
EMBL; AL133248; CAB66108.1;
EMBL; AK117942; BAC42580.1;
EMBL; BT005376; AAO63440.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakajima M., Enju A., Kamiya A., N
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
Seki M., Iida K., Sa
                                                                                                                                                                                                                                                                 PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCCl_2; 1.
Cell wall; Glycosidase; Hydrolase; Sign:
SEQUENCE 431 AA; 46572 MW; 0F0F30DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palm C.J., Quach H.L., Sak
Tang C.C., Toriumi M., Won
Shinozaki K., Davis R.W.,
"Arabidopsis ORF clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., I Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Lie J.M., Lin J., Miranda M., Narusaka M., Nguyen lee J.M., Lin J., Miranda M., Narusaka M., Nguyen l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    T46187; T46187.
                 174
                                           108
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I.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam
M., Lin J., Miranda M., Narusaka M., Ngyen M., Onodera C.S
J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.
C. Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan Saki K., Davis R.W., Theologis A., Ecker J.R.;
donnais OPP Cloner ".
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             INGNGOVWWPSSCKINKSLPCRDAPTALTFWNCKNLKVNNLKSKNAQQIHIKFESCTNVV
                                        GKTYLLKSTRERGECKSLRNFQILGTLSASTKRSDYKDKNHWLILEDVNNLSIDGGSTGI
                                                                                                                          SKNIESNNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPK
                                                                                                                                                                                  SILLLIIIFASSISTCRSNVID---
                                                                 NKNYLLKQITESGECRSSISVKIFGSLEASSKISDYKDRRLWIAFDSVQNLVVGGG--GT
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                                                                                                                                                       AVFLCVLLMLSLCKALSSNVDDGYGHEDGSFESDSLLKLNNDDVL---
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.X., Queti
 (NOV-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                metabolism;
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                                                                                                                                                                                                               Mismatches 116;
Narusaka
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                                                                                                                                                                                                                                                                                  Signal
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8.7e-66;
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ka M., Carninci
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Kawai
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01-JAN-1998
01-JAN-1998
01-JUN-2003
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MEDLINE=20083487; PübMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Xoo H., Moffat K.S.
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venner J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
                                                                                                                                                                                                                                                   GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:bydrolase activity, acting on glycosyl
GO; GO:001650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; pbH1.
InterPro; IPR006826; pbH1.
InterPro; IPR008626; pbH1.
SMART; SM00710; PbH1; 5.
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                                                                                                                                                              PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1.
Cell wall; Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Columbia;
                        Conservative
                                                                                                                                         AA;
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                                                                                                                                         45924 MW;
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                                                                                                                      Hydrolase.
24 MW; F756754C0390A80B CRC64;
                  74;
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                                             5.5; DB 10;
4.8e-65;
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cummitted (MAR-1996) to the EMBL/GenBank/DDBJ datab
-! SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HY;
CC (POLYGALACTURONASES).

DR EMBL; X95800; CAA65072.1; -.

DR GO; GO:0005618; C:cell wall; IEA.

GO; GO:0016799; F:hydrolase activity, acting on glycc
DR GO; GO:0016799; F:hydrolase activity; IEA.

DR GO; GO:000450; F:polygalacturonase activity; IEA.

GO; GO:000459; F:polygalacturonase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR000743; Glyco hydro_28.

InterPro; IPR000740; Reg_chr condens.

PR Pfam; PF00295; Glyco_hydro_28; 1.

R SMART; SM00710; PbH1; 6.

R PROSITE; PS00502; POLYGALACTURONASE; 1.
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01-JUN 2003 (TrEMBLrel. 24,
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FAMILY 28 OF GLYCOSYL HYDROLASES
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STRAIN=cv . Maravilla;
MEDHINE=94302167; PubMed=8029352;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Prunus persica) endopolygalacturonase -
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ysiol. 105:225-231(1994).
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Q8VXT3;
01-MAR-2002
01-OCT-2002
01-JUN-2003
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SMART; SM00710; PBH1; 6.
PROSITE: become
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InterPro; IPR006626; PbH1.
InterPro; IPR000408; Reg_chr_condens
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GO:0006798; F:bydrolase activity,
GO:0004650; F:polygalacturonase ac
GO:0005975; P:carbohydrate metabol
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1; Glycosidase; Hydrolase.
458 AA; 49716 MW; E7BABB
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49716 MW; E7E
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Pred. No. 1
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      Matilla
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Brassica rapa (Turn.p).

Bukaryota; Viridiplantae; Streptophyta; Embryomermatophyta; Magnoliophyta; eudicotyledons;

Shermatophyta; Magnoliophyta; erassicaceae; Brass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALQKHLVLFYVVVSFCAASCYSSGFQEVNSLHSFVDH--EKESGYNSRAHPSNMNTIEG
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TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                             - QNARAKCNNVKPAYKGAVSPRCS
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Last annotation updat
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      Brassica
                                             Embryophyta;
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                                               Tracheophyta;
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during pod development in oilseed rape (Brassica napus L.)."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES

(POLYGALACTURONASES)

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Best Local S
Matches 222
                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid. eurosids II; Brassicales; Brassicaceae; Brassica. MCBI TaxID=3708;
                                                                                                                                                                                                                                                                                     Q42636;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (COLYGALACTURONASES).

EMBL; AJ428543; CAD21651.2; -- E.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0004575; P:carbohydrate metabolism; IEA.
                               SEQUENCE FROM N.A.
Jenkins E.S., Paul
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InterPro; IPR000408; Reg chr condens.
Pfam; PF00295; Glyco hydro 28; 1.
PROSITE; PS00502; POLYGALACTURONASE; 1.
PROSITE; PS00626; RCC1 2; 1.
Cell wall; Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                          Polygalacturonase
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       Characterization and
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Pred. No. 2.
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     ., Roberts J.A.; polygalacturonase
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QRSTPE ID QRSTP AC QRSTP AC QRSTP DT 01-MA DT 01-OC DE POLYG GN PC-PG OS PYTUS OC EUKAZ OC SPERM OC GUS NCBI RN [1]
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Best Local
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Q8GTP8;
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01-MAR-2003 (TrEMBL
01-OCT-2003 (TrEMBL
Polygalacturonase p
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PROSITE; PS00626; RCC1 2; 1.
Cell wall; Glycosidase; Hydrolase; Signal.
SIGNAL 1 25 POTENTIAL.
CHAIN 26 433 POLYGALACTURO
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InterPro; IPR006626; pbH1.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 6.
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GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on g:
GO; GO:0016798; F:polygalacturonase activity; IEA.
GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                   PC-PG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGGG--GTINGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNNIDKVDKNGIKVINVLSFGAKGDGKTYDNIAFEQAWNEACSSRTPVQFVVPKNKNYLL
                                                                                                                                                                                                                                  ----GKASCKNVNVKDKGTVSPKC
                                                                                                                                                                                                                                                           SGKPSEATCKNVHFNNAEHVTPHC 442
                                                                                                                                                                                                                                                                                    QNYCDK-DKCEQQESAVQVNNVVYRNIQGTSATDVAIMFNCSVKYECQGIVLENVNIKG-
                                                                                                                                                                                                                                                                                                            QNYCDRVEPCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEGIIMENINLVGE
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433 AA;
                                                                                                        (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                                PRELIMINARY;
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                              Rosaceae;
                                         Streptophyta; Embryophyta; Tracheophyta;
/ta; eudicotyledons; core eudicots; rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1103; DI
Pred. No. 3.2e
70; Mismatches
                                                                                             Last sequence up
Last annotation
(EC 3.2.1.15).
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POLYGALACTURONASE.
39BE624426D26739
                                                                                                                                                                PRT;
                              Maloideae; Pyrus
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Matches 224
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Kubo Y.
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Hiwasa K., 1
                                                                                                                                                                     065886;
01-AUG-1998
01-AUG-1998
01-JUN-2003
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InterPro; IPR000626; PbH1.
InterPro; IPR000626; PbH1.
InterPro; IPR000408; Reg_chr_condens
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
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GO; GO
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Submitted
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SIGNAL 1 24 PC
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                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids I; Rosales; Rosaceae; Rosoideae; Rubus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00502; POLYGALACTURONASE; PROSITE; PS00626; RCC1_2; 1.
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                                                                            Rubus idaeus (Raspberry).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                         065886
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                                                                                                                                                 Polygalacturonase
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GO:0016798; F:hydrolase activity, acting on gl
GO:0004650; F:polygalacturonase activity; IEA.
GO:0005975; P:carbohydrate metabolism; IEA.
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24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKNAQQIHIKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIAFDSVQNLVVGGGGTINGNGQVWWDSSCKINKSLPC-RDAPTALTFWNCKNLKVNNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                       IKFDCSTNFPCEGIIMENINLVGESGKPSEATCKNVHFNNAEHVTPHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAWKAACSSSGAIVLVVPQ-KKYLVRPIDFSGPCKSQLTVQIYGTIEASEDRSIYKDIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEGLKFMELIRPRTQLSSSRKLNTI-TGGIATSSAPAKTISVDDFGAKGNGAD-DTQAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALKTQLLWSFVVVFVVSFSTTSCSGSSFQEVNALHSYVDHVDDRVSGYNSRAYPSYMDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVIQRNSILLLIIIFASSIST--CRSNVIDD-NLFKQVYDNILEQEFAHDFQAYLSYLS-
                                                                                                                                                                                                                                                                                                                                                                                              ITLNCSQSVPCRGIALQSVRL--QNGR---AECNNVQPAYKGVASPRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQASNIKFLNVENQDVKYPIIIDQNYCD-RVEPCIQQFSAVQVKNVVYENIKGTSATKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSGSONVOATNITCGPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQDAQQMHVRFQNCINVQASRLTVTAPEDSPNTDGIHVTNTQNITISSSVIGTGDDCISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSGSQRVQATDITCGFGHGISIGSLGEDGSKDHVSGVCVNGAKLSGTSNGLRIKTWQGGS
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(MAY-2002) to the EMBL/GenBank/DDBJ databases
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. La France;
, Kinugasa Y.
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., Amano S., Hashimoto A.,
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07, Last sequence up
24, Last annotation
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Pred. No. 3.2e-62;
9; Mismatches 132;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR000626; PbH1.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ224147; CAA11846.1; -.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl
GO; GO:0004650; F:polygalacturonase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
[1]
STRAUNECY FROM N.A.
STRAUNECY Glen Clova; TISSUE=Fruit;
Jones C.S., Davies H.V., McNicol R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of three genes up-regulated (Rubus idaeus cv. Glen Clova).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POLYGALACTURONASES
                                                                                                                                                                                                                                                                                      112 VVPKNKNYLLKQITFSGPCRSSISVKIFGSLEASSKISDY-KDRRLWIAFDSVQNLVVGG
306
                         408
                                                   246
                                                                              350
                                                                                                                                    290
                                                                                                                                                              126
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                                                                                                                                                                                                                                                                                                                            208;
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                                                                                                                                                                                                                                                                      7 LVPK-KNYLVKPITFSGPCKSKLTMQTYGSIEASDDRSVYSKDLYHWIIFDNVRNLLVQG
                                                                                                                                                                                                                                     GGTINGNGQVWWPSSCKINKSLPCRD-APTALTFWNCKNLKVNNLKSKNAQQIHIKFESC
                         IIMENINLVGESGKPSEATCKNVHFNNAEHVTPHC
                                                                             DVKYPIIIDQNYCDRVE--PCIQQFSAVQVKNVVYENIKGTSATKVAIKFDCSTNFPCEG
                                                                                                         GPGHGISIGSLGEGGSEDRVSKVTVNGAKISGTMNGVRIKTWQGGSGMASNIVFQNIEMN
                                                                                                                        GPGHGISIGSLGSGNSEAYVSNVTVNEAKIIGAENGVRIKTWQGGSGQASNIKFLNVEMQ
                                                                                                                                                             TNVQASYLTVTAPETSPNTDGIHVANTQNITISNSIIGTGDDCISIVSGSQNVQASSITC
                                                                                                                                                                               TNVVASNIMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDDCISIVSGSQNVQATNITC
                                                                                                                                                                                                                  PGTINGNGQIWWQNSCKNKHTKPCGTLAPTAVTFYQCNNLVVKNLKFKDSQQMHVSFEDC
                                                   DVTNPIIIDQNYCDTSDKRKCKQQSKAVKVQNVLYKNIRGTSASKYAIAFDCSKSIPCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FEB-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                335
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                36432 MW;
                                                                                                                                                                                                                                                                                                                                        44.4%;
62.1%;
 HKRAKCSNVNLAYKENVSPRC
                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                          Score 1061.5;
Pred. No. 1.2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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444443990000000000000000000000000000000	Score
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	of purified PG beta-s 5389-90) were used for eta-subunit cDNA clone onsensus DNA sequence -2003 to correct PN fi	ish.	contg. lowered levels of pol f tomatoes less susceptible t inactivate poly-galacturonas				5.	ίω			n/Qualifiers "unknown"		polygalacturonase; tomato; pathogen	fragment.			10 AA.	ALIGNMENTS	AAW80371 ABB934678 AAY117484 ABB215282 ABB61097 ABB33329 ABU70397 AAW37483 AAW93864 ABB83328 AAW93864 ABB83328 AAW63114 ABB84176 ABB64176 ABB73597 ADB07280 ADB
	ubunit was performed. the construction of s and fragments of 11 obtained is given in eld.)		polygalacturonase le to pathogens and onase activity.										·						Aaw80371 Vasopress Abp34678 Human ORF Aay17484 Human Nix Abj25282 Mouse BAC Abb61097 Drosophil Abb83329 Murine TS Abu70397 Human adi Aay17483 Murine NI Aaw93864 Human BNI Abw93864 Human ENI Abb83328 Human TSA Abb64176 Drosophil Abb73597 Candida a Abb64176 Drosophil Abp73597 Candida a Adb07282 Alloiococ Adb07282 Alloiococ Adb07282 Alloiococ Adb81952 Pea bligh Abb73163 Drosophil Abp73597 Candida a Adb07280 Alloiococ Adb07280 Alloiococ Adb93381 C. albica Abb36839 Protein e

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                                                                                                                                                                                                                                                                                                                                        AAW10696 and AAW10697 are internal peptides of the beta subunit of tomato polygalacturonase isoform 1 (PG1). The two peptides were generated by digestion with Lys-C and Gly-C endoproteases respectively. The peptides were used for the design of degenerate PCR primers used for CDNA library screening. A cDNA molecule encoding PG1 was identified, this sequence was used to produce constructs, antisense to the PG1 coding sequence, which are used to transform a tomato plant cell so as to reduce or eliminate PG1 activity. There are two isoforms of tomato polygalacturonase (PG), PG1 and PG2. PG1 has a much higher heat stability level (usually at least by 20 deg. C.) than PG2. By reducing or eliminating PG1 expression, leaving the less heat-tolerant isoform PG2. The process for production of tomato pastes, sauces etc. becomes less costly due to a lower temperature being needed for PG breakdown. A higher viscosity is also produced due to increased soluble pectin content. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic tomato plants with low level of polygalacturonase isoform 1 have higher content of soluble pectin(s) and require less heat energy teliminate polygalacturonase activity of the fruit.
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                                                                                                                          Best Loc
Matches
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                                                                                                                                                                                                                                                     Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Col 9; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polygalacturonase beta-subunit peptide produced after Lys-C digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DELL/) DELLAPENNA D. (WATS/) WATSON C F.
                                                                                                                                                           Local
                                                                                                                          Similarity 100 10; Conservative
                                                           1 NGNGANGOXV 10
NGNGANGQXV 10
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                                                                                                                96.0%; but
100.0%; Pr
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                                                                                                                          Score 48; DB; Pred. No. 0.1
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                                                                                                                                                                                         Length 10
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RESULT 4 AAB48353 ID AAB4

AAB48353 standard; peptide; 10 AA

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ABP35664
ID ABP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a new method for modifying pectin that involves providing a host having pectin methylesterase (PME) activity and polygalacturonase (PG) activity, transforming the host by silencing PG activity to provide an increased PME to PG ratio, preparing a PME extract from the transformed host, and using the PME extract to modify pectin. A PME modified pectin is useful for foodstuffs preparation, and to impart an increased functionality to food products such as yogurt, milk/fruit juice and whey drinks. PME is useful to reduce the number of ester groups in a pectin in a high-ratio manner and to descript, which were the products in the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifying pectin, for foodstuffs preparation, involves transforming host having pectin methylesterase (PME) and polygalacturonase (PG) activity by silencing PG activity, to increase PME to PG ratio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200078982-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a pectin in a block-wise manner, and to de-esterify two or more adjacent galacturonic acid residue of a pectin on at least substantially all of the pectin chains. The present sequence represents an internal peptide fragment of the PG enzyme, used for designing primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Christensen TMIE, Kreiberg JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1999;
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Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 42; 78pp; English.
                                                                                                         Fungal
                                                                                                                                                                24-JUL-2002
                                                                                                                                                                                                                                                                    ABP35664 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-091573/10.
                                                                                                              ZBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            NGNGANGQXV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGNGANGOXV 10
                                                                                                            protein sequence #90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                (first
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                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                       979
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Pred. No.
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  erolaemic; lovastin;
ergot alkaloid; ergotamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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RESULT 6 AAB70839

AAB70839 standard; protein; 321 AA.

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06-AUG-2003 25-JUN-2001

(revised)
(first entry)

S. halstedii

cellulase protein.

Cellulase; fusion construct; protein synthesis; papermaking; glyceraldehyde phosphate dehydrogenase; food industry; feed washing composition; catalyst.

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metabolite by a fungus. This involves modulating the expression of at CC least one ZBC (zinc binuclear cluster protein) gene in a manner to CC improve the yield of the secondary metabolite. Methods of the invention CC may be used for improving the production of the secondary metabolite e.g. CC antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), CC an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, CC a fungal toxin, a modulator of cell surface receptor signalling, a plant CC growth regulator, a pigment, an insecticide, or an antinepplastic CC compound. The method results in a decrease in fermentor run-time, a CC decrease in the size of the secondary metabolite, or an antinepplastic CC compounds. The method results in a decrease in fermentor run-time, a CC equivalent amounts of the secondary metabolite, or an antinepplastic CC waste that must be handled in downstream processing. The sequences given in records ABP3557-ABP35722 represent ZBC proteins. Note: The sequence CC data for this patent did not form part of the printed specification, but fig. wispo.int/pub/published_pot_sequences
             Matches
                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antineoplastic the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200224865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                     Sequence 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 192; 49pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New method for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to improving the production of a secondary
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          Similarity 7; Conserv
                Conservative
                                                                                                                                            ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improving the production of a secondary metabolite e.g. agent, ergot alkaloid from a fungus involves modulation of at least one zinc binuclear cluster protein gene.
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                                              80.0%;
J*,
J. 0*;
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                                              Score 40;
Pred. No.
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                    Mismatches
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                                              DB 5; L
                                                                         Length 979;
                    Indels
                    0,
                    Gaps
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RESULT 7
AAW18210
ID AAW1
XX AAW1
AC AAW1
XX
DT 25-W
DT 29-S
XX
DE Cell
XX
KW Endc
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OS Cel:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This invention describes a novel microorganism (A) of the genus Ashbya CC for biotechnical production of proteins (I), containing a genetic CC construct so that the protein-synthesis capacity is altered relative to CC the wild-type species A. gossypii ATCC 10895. The invention also CC describes (1) cellulase gene (IIa), for use in (A), having a sequence, CC from Streptomyces halstedii; (2) promoter (P) and transcriptional CC terminator (TI) from the sequence encoding the glyceraldehyde phosphate CC dehydrogenase of A. gossypii; (3) genetic structure containing (IIa) plus cregulatory regions that provide expression in Ashbya; (4) a vector CC containing (IIa), P and/or TT, or the structure of (3), plus signals that provide replication in host cells or integration into a cellular genome; (5) transformed Ashbya, for production of cellulase, containing the gene copy producing (A) by exchanging the promoter and/or increasing the gene copy contacture of (3) in replicable form; (6) producing gene; and (8) (I) produced by the method of (6). (A) are used for recombinant production of cellulase, useful in comparanking, medicine, food/feed industries, washing compositions and/or cascatalysts. (A) provide higher protein yields than wild-type cells. CC in the construction of the A. gossypii/S. halstedii genetic construct cused to illustrate the method of the invention. (Updated on 06-AUG-2003 CC correct OS field.)
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
                                Endoglucanase; cenA gene; cellulase; cellulose; glucose
                                                                                                      25-MAR-2003
29-SEP-1997
                                                                                                                                                        AAW18210;
                                                                 Cellulomonas fimi endoglucanase
                                                                                                                                                                                  AAW18210 standard; protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified Ashbya organisms with altered protein production properties, useful particularly for production of Streptomyces halstedii cellulas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Althoefer H, Pompejus M, Benito R, Santamaria R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         correct OS field.)
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                                                                                                                                                                                                                                                                      256 NGNGSNGE 263
                                                                                                                                                                                                                                                                                                     1 NGNGANGO 8
                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
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Fernandez
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Pred. No. 1.2e+02;
2; Mismatches 0
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18-DEC-1990;
19-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence (AAW18210) of a Cellulomonas fimi endo-1,4- beta-glucanase (EC-3,2.1.4) was deduced from an isolated DNA fragment (AAT71711) contg. the cenA gene. The enzyme is capable of hydrolysing beta-1,4-glycosidic linkages in the interior of a cellulose molecule, converting the cellulose to glucose. The C-terminal region of the enzyme is crucial for activity; deletion of 12 amino acids from that end results in loss of all activity. Recombinant endoglucanase can be expressed in host cells, esp. E. coli, utilising vectors incorporating the cenA gene. (Updated on 25-MAR-2003 to correct PF field.)
23-MAR-2001; 2001WO-US009231.
                       27-SEP-2001
                                             WO200171042-A2
                                                                     Drosophila melanogaster
                                                                                            pharmaceutical
                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 9876
                                                                                                                                                        26-MAR-2002
                                                                                                                                                                              ABB61028;
                                                                                                                                                                                                  ABB61028 standard; protein; 427
                                                                                                                                                                                                                                                                                                                                                         Sequence 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5A-F; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloned Cellulomonas fimi cenA gene - conversion of cellulose to glucose.
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N-PSDB; AAT71711.
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Peptide
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90US-00630396.
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Pred. No. 1.7e+02;
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 9876; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLO5 protein; ZmMLO5; chromosome 3; mutation; recessive allele; disease resistance; pathogen; anti-infective; antipathogenic; antiviral; antifungal; antihelminthic; anti-arthropod; maize; HvMLO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize MLO5
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                                                                           07-JUL-1998;
                                                                                                                           07-JUL-1999;
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                             (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ention relates to an isolated nucleic acid detection of detecting 1000 or more genes from Drosophila. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNGANGNHV
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2000US-00614150
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                                                                                                                                                                                                                                                                         /label= Transmembrane_helix 62. .149
/label= C-terminal_region
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the maize MLO5 (ZmMLO5) protein, which exhibits sequence homology to barley MLO1 (HvMLO1) sequence. MLO5 protein is encoded by a mutation-induced recessive allele MLO5, located on chromosome 3, that confers resistance to plant pathogens. Expression of native MlO genes in plants can be altered by transforming them with a DY
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genes from Drosophila and
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Pred. No. 1.2e
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The invention relates to an isolated nucleic capable of detecting 1000 or more genes from

acid detection reagent Drosophila. The invent

invention

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Disclosure; SEQ ID NO 10272; 21pp + Sequence Listing; English.

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                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide that encodes nacrein. The methods and compositions of the present invention are useful for pearl oyster cultivation and pearl formation. The present sequence represents the amino acid sequence of Pinctada maxima nacrein.
                                                                                                                                                                                                                   Sequence 568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24-25; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and polypeptide from the nacre gene of the Pinctada margaritifera species, useful for pearl cyster cultivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang
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(HSIE/) HSIEH-LI H M.
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                                                                                                   l Similarity
6; Conserva
                                                   1 NGNGANG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NGNGANGQ 8
NGNGSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li H,
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pearl oyster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hsieh-Li
                                                                                                                                74.0%;
85.7%;
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                                                                                                      1;
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                                                                                                                                Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cultivation; pearl formation.
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Pred. No. 3.6e+02;
                                                                                                   Mismatches
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                                                                                                                                   DB 6;
4.7e+02;
                                                                                                         0
                                                                                                                                                          Length 568;
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                                                                                                      Indels
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 12

WO200277183-A2.

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RESULT 13
ABU15903
ID ABU15
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ABU15903
AC ABU15
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DT 19-JU
DT 19-JU
DX
DE Prote
XX
XW Antis
XX
OS Staph
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                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and interactions.
                         Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                    Antisense;
                                                                                                     19-JUN-2003
                                                                                                                               ABU15903;
                                                                                                                                                       ABU15903 standard; protein;
                                                                                                                                                                                                                                                                                                                        Sequence 582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                               from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                             printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 5238; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 5238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB59482;
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                                                                                                                                                                                                                     440 NGNGSNG 446
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                                                                                                                                                                                                                                            1 NGNGANG 7
                                                                             encoded
                                                                                                                                                                                                                                                                      Similarity 6; Conserv
                                                  prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP NY.
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                    (first entry)
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                                                                            by Prokaryotic
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582
                                                                                                                                                        1038
                                                                                                                                                                                                                                                                      Score 37; DB
Pred. No. 4.8e
1; Mismatches
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                                                                             essential
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, 4.8e+02;
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                                                                             #1430
                                                                                                                                                                                                                                                                                              Length 582;
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RESULT 14
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AC ABB83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC polypeptide or its fragment whose expression is inhibited by the CC antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits gene product lies or agene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of Strains; or (13) identifying the target of a compound that inhibits the CC proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational contents.
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242; 06-5EP-2001; 2001US-00948993; 25-0CT-2001; 2001US-0342923P; 08-FEB-2002; 2002US-0362699P; 06-MAR-2002; 2002US-0362699P;
                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002
                                                                                                                                                                                                                                                                                                  Sequence 1038 AA;
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                                           ABB83327
                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e invention relates to an isolated nucleic acid comprising any one of e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                              1 NGNGANGQXV
                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELITRA PHARM INC.
                                        standard; protein; 141 AA.
                                                                                                                                         DGNGKNGQII 511
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 43827; 1766pp; English.
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                              10
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Carr GJ,
                                                                                                                                                                                                                                       74.0%;
                                                                                                                                                                                                                     2
                                                                                                                                                                                                                     Score 37; DB 6;
Pred. No. 8.7e+02;
2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen
Forsyth
                                                                                                                                                                                                                                                           Length 1038;
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Xu HH;
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ABR52643
ID ABR5
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for identifying a compound (1) that inhibits binding of TSAP (Tumour Suppressor Activated Pathway) 6 to a TSAP6 binding protein. The present sequence is one such TSAP6 binding protein. (1) are useful for modulating tumour reversal and/or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000FR-00017027
18-SEP-2001; 2001WO-FR002896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200252274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuroprotective; cytostatic; TSAP6; apoptosis; cancer; neurodegeneration; Tumour Suppressor Activated Pathway 6; TSAP6 binding protein; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine TSAP6 binding
                                                                                                                                                                                                                                                                                                                                                          Sequence 141
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-2002
                                                                                                                       Saccharomyces
                                                                                                                                          Multiprotein
                                                                                                                                                             Protein sequence #SEQ ID 151.
                                                                                                                                                                                                                          ABR52643 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-508914/54.
Bauer A,
                                                            20-DEC-2001;
                                                                                20-NOV-2002
                                                                                                    EP1258494-A1
                                                                                                                                                                                  20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                              for treating cancer or neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds that inhibit binding of TSAP6 to proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR ENGINES LAB
                    (CELL-) CELLZOME AG
                                       15-MAY-2001; 2001EP-00111774
                                                                                                                                                                                                                                                                                                                            Local
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 Gavin A,
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                           AA,
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                                                            2001EP-00130253
                                                                                                                                          complex; eukaryote; drug target; diagnosis
                                                                                                                                                                                 (first entry)
                                                                                                                        cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                         79pp; French.
                                                                                                                                                                                                                                                                                                10
  Grandi P,
                                                                                                                                                                                                                                                                                                                            72.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                    0;
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Pred. No.
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  Krause
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; 1.6e+02;
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  Kruse
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   BD;
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Search completed: July 21, 2004, 17:06:23 Job time: 5.07709 secs
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                                                                                                                                                    Query Match 72.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                       The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                        Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 151; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, protein a drug target in the treatment or prevention of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-250078/25.
N-PSDB; ACC60685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder.
                                                                                62 NGNGGNG 68
                                                                                                                   1 NGNGANG 7
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                                                                                                                                                                             72.0%;
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                                                                                                                                                                          Score 36; DB 6;
Pred. No. 2e+02;
                                                                                                                                                              Mismatches
                                                                                                                                                          1.
                                                                                                                                                                                             Length 175;
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Result
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Maximum Match 10
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        2254
226
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276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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seq
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length: 2000000000
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US-09-347-639-10
US-09-240-639-10
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•	μ	Sequence 17, Appl		Sequence 17, Appl	Sequence 15, Appl	•	Sequence 101, App	•	-	-		Sequence 16, Appl	-	•	•	-	Sequence 34, Appl

ALIGNMENTS

## RESULT 1 US-08-273-538A-1 Sequence 1, Application US/08273538A Patent No. 5569831 GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Microsoft Word CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/273,538. FILLING DATE: CLASSIFICATION: 800 CLASSIFICATION: 800 TELEFAX: 608/251-9166 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 aming acids ATTOKNEL, Seay, NICHOLL 27386 REGISTRATION NUMBER: 27386 TELECOMMUNICATION INFORMATION: 608/251-5000 777-9166 TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: internal ORIGINAL SOURCE: APPLICANT: DellaPenna, Dean TITLE OF INVENTION: Transger TITLE OF INVENTION: Altered CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: COUNTRY: USA ZIP: 53701-2113 STREET: P.O. I ORGANISM: Lycopersicon esculentum ADDRESSEE: amino acid Wisconsin Nicholas J. Seay O. Box 2113 Transgenic Tomato Plants with Altered Polygalacturonase Iso US/08/273,538A Isoforms

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1 NGNGANGQXV

Matches Query Match Best Local

10;

Conservative

Similarity

100.0%; \*\*

96.0%; Score 48; 100.0%; Pred. No.

DB 1; 0.041;

Length 10;

Mismatches

0,

Gaps

NGNGANGOXV 10

Sequence 1, Application US/08632806A Patent No. 6127179

GENERAL INFORMATION:

08-632-806A-1

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US-09-286-691-27
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                                                                                                                                                                                                                        Sequence 27, Application US/09286691 Patent No. 6190189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                        FILE REFERENCE: 42-96
CURRENT APPLICATION NUMBER: US/09/286,691
CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
             EARLIER APPLICATION NUMBER: US 60/027,883
EARLIER FILING DATE: 1996-10-04
EARLIER APPLICATION NUMBER: PCT US97/18008
EARLIER FILING DATE: 1997-10-03
                                                                                                                                             APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Cellulases
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/632,806A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DellaPenna, Dean
APPLICANT: Watson, Colin F.
TITLE OF INVENTION: Gene Promoter for Tomato Fruit
NUMBER OF SEQUENCES: 8
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Pred. No.
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Query Match
Best Local Similarity
Freches 6; Conserve
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                             ; FEATURE:
; OTHER INFORMATION: Mlo5
US-09-347-650-8
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CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/027,883
PRIOR FILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: PCT US97/18008
PRIOR APPLICATION NUMBER: 09/286,691
PRIOR APPLICATION NUMBER: 09/286,691
PRIOR FILING DATE: 1999-04-05
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
TITLE OF INVENTION: Manipulation of Mlo Genes to Enhance Disease Resistance
TITLE OF INVENTION: in Plants
TILE REFERENCE: 5718-42035718/158714
FILE REFERENCE: 5718-42035718/158714
CURRENT FILING DATE: 1999-07-06
RUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                            SEQ ID NO 8
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Patent No. 6268198
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APPLICANT:
Query Match
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                                                                          TYPE: PRT
ORGANISM: Zea mays
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Chen, Huizhong
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 Score 37;
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 DB 4;
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RESULT 6
US-08-811-492-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/496,247
EILING DATE: 28-UUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
APPLICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\Dos/Ms\Dos
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MODIFIED PROTEINS, METHODS TITLE OF INVENTION: PRODUCTION AND METHODS FOR TITLE OF INVENTION: PROTEINS
STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                 TELEFAX: 509-927-1705
                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                               i: 19 amino acids amino acid
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                                        3S: single
linear
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                                                                                                                                                                                                                  127:
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1; Mismatches
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PURIFICATION OF TARGET
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                                                   Matches
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                                                                 Best
                                                                             Query Match
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Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,910
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                  TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                        LIBRARY:
CLONE: 1
                                                                Local Similarity
                                                                                                                                                            TYPE: STRANDEDNESS: SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                     LENGTH:
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STREET: 3174 Porter Drive
49
                         1 NGNGANG 7
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NGNGKNG
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IBM Compatible
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                                                                                                                                                                             single
                                                                 70.0%;
85.7%;
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                                                                 Score 35; DB 2;
Pred. No. 1.3e+02;
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                                                      Mismatches
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                                                                              Length 232;
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                                                      Indels
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                                                     Gaps
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; Sequence 1, Application US/09199892
; Patent No. 6307021

RESULT 8 US-09-199-892-1

GENERAL INFORMATION:

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Query Match
Best Local Similarity
Watches 6; Conserve
; TYPE: PRT; ORGANISM: P. sativum US-09-240-639-10
                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-240-639-10
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                                                                                                                                                                    Sequence 10, Application US/09240639
Patent No. 6350447
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: MCTHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
                                                   FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
LENGTH: 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Wir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 1715374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN APOPTOSIS REG
TITLE OF INVENTION: ULATOR
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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1715374
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85.7%;
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 232;
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GENERAL INFORMATION:
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                                                              Matches
                                                                                              Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              ATTORNEI/ Lee Cheng
RAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 98-0
TELECOMMUNICATION INFORMATION:
THIRPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: September 10, 1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                            Local Similarity 85.7%; nes 6; Conservative
                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2033 K St
CITY: Washington
STATE: D.C.
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OPERATING SYSTEM:
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                                                                                                                                                  IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 TOPOLOGY:
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71 NGNGASG
                                1 NGNGANG 7
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                                                                                                                                                                                                                                                                                                               574 amino acid residues
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KOJÍ YANAI et al.

JENTION: -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
JENTION: ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCING
JENTION: -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
                                                                                                                                                                                                                                                             NO. 6337201 relevant
                                                                                                                                                                   mat peptide
1 .. 574
                                                                                                                                                                                                                Microorganism:
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                                                                                                                                                                                                                                               protein
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75.0%;
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                                                                                                                                                                                                               Scopulariopsis brevicaulis IFO4843
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                                                               Score 35; DB 4; Length 574; Pred. No. 3.4e+02; 1; Mismatches 0; Indels
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Pred. No. 2.7e+02;
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RESULT 11 US-09-508-264A-3 ; Sequence 3, Application US/09508264A ; Patent No. 6566111

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APPLICANT: NAKANE, Akitaka

APPLICANT: KONO, Toshiaki

TITIE OF INVENTION: Beta-Fructofuranosidase And Its Gene
FILE REFERENCE: 2000-0267*/LC/00144

CURRENT APPLICATION NUMBER: US/09/508,264A

CURRENT FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/JP98/04087

PRIOR APPLICATION NUMBER: DP/245154/1997

PRIOR APPLICATION NUMBER: JP/245154/1997

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 17
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US-09-268-347-34
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; SEQ ID NO 28
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-28
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US-09-268-347-28
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Best Local Similarity
Matches 6; Conserva
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Patent No. 6335182
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
ETIT DECEDENCE. 1028-66
                                                                                                                                                                                          Sequence 34, Application US/09268347
Patent No. 6335182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 1104
                                                                                                                                                                          GENERAL INFORMATION:
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                                                    APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
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CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
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NAME/KEY: mat peptide
LOCATION: (1)...(613)
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TYPE: PRT
ORGANISM: Scopulariopsis brevicaulis IFO4843
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85.7%;
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Pred. No. 3.7e+02;
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Best Local Similarity
"-+rhes 6; Conserv:
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5178861-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Haemophilus influenzae US-09-268-347-34
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;NUSSENZWEIG, RUTH S.;NUSSENZWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF CIRCUMPOROZOITE PROTEINS NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Patent No. 5178861
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Patent No. 5756343
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Best Local
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 26-NOV-1:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/
FILING DATE: 22-JUN-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WU, CARL; CLOS, JOACHIM;
APPLICANT: WESTWOOD, J. TIMOTHY:, RABINDRAN,
TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-JAN-1994
                                                                                                                                                                                                                                                               CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
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Local Similarity 85.7%;
les 6; Conservative
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                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 11
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                                                                                                                                                                                                                                                                                                 345 PARK AVENUE
                                                                                                                                                                                                                                                USA
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                   26-NOV-1990
                                                                                                                                                                                              FLOPPY DISK
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85.7%;
                                                                                                       US/08/178,477B
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Pred. No. 6.7e+02;
0; Mismatches 1
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 2026-4103US1
REFERENCE/DOCKET NUMBER: 2026-4103US1
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 50
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: peptide
US-08-178-477B-16
Query Match
Best Local Similarity 60.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps
Oy 1 NGNANGGXV 10
|| | | | | | |
Db 18 NGNPANGSNI 27

Search completed: July 21, 2004, 17:09:28
Job time: 1.62099 secs
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Result
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Maximum DB seq length: 200000000
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Maximum Match 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
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                                                                                                                                                                                                                                                                                                                       No
                                                                                                                                                                                                                                                                                                                                                                                                                 score greater than and is derived by
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                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          July 21, 2004, 17:08:27 ; Search time 1.73448 Seconds (without alignments) 1802.048 Million cell updates/sec
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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187
260
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388
5688
1038
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763
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US-10-149-310-192

US-10-425-114-53903

US-10-425-114-44021

US-10-425-114-44021

US-10-427-963-201301

US-10-424-599-150886

US-10-086-510-5

US-10-086-510-5

US-10-282-122A-43827

US-09-949-029-70

US-09-949-029-70

US-10-425-114-44598

US-10-425-114-44598

US-10-424-599-145867

US-10-156-761-12117
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                                Sequence 4414, App
Sequence 284, App
Sequence 192, App
Sequence 53903, A
Sequence 56925, A
Sequence 56925, A
Sequence 201301,
Sequence 150886,
Sequence 150886,
Sequence 70, Appli
Sequence 70, Appli
Sequence 70, Appli
Sequence 70, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 71, Appli
                                                                                                                                                                                                                                                                                                                 Description
                    Sequence
  145867,
12117, A
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#### ALIGNMENTS

RESULT 1 US-10-369-493-4148

Sequence 4148, Application US/10369493 Publication No. US20030233675A1

IN PLANTS FOR PRODUCTION OF

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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4148
LENGTH: 451
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                                                                                                                                                US-10-369-493-4148
                                                                        Matches
                                                                                                           Query Match
                                                                                                                                                                                 NAME/KEY: unsure LOCATION: (1)...(
                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Neurospora crassa
FEATURE:
                                                                                         Local
 277
                                   1 NGNGANGQ 8
                                                                      l Similarity
7; Conserv
NGNGASGQ 284
                                                                        Conservative
                                                                                                                                                                                     (451)
                                                                                                                                                                unsure at
                                                                                         80.0%;
87.5%;
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                                                                  Score 40; DB 15; L
Pred. No. 1.1e+02;
Mismatches 0;
                                                                                                       Length 451;
                                                                        Indels
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Sequence

US-09-801-368-284

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Sequence 192, Application US/10149310

Publication No. US20040077039A1

GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary

APPLICANT: Sherman, Amir

ITILE OF INVENTION: Modulation of Secondary Metabolite Production by

TITLE OF INVENTION: Zinc Binuclear Cluster Proteins

FILE REFERENCE: 14184-019US1

CURRENT APPLICATION NUMBER: US/10/149,310

CURRENT APPLICATION NUMBER: PCT/US01/29288

PRIOR APPLICATION NUMBER: PCT/US01/29288

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19
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                                         Query Match
Best Local Similarity
"herhes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-149-310-192
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                                                                                                                                            US-10-149-310-192
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 192
LENGTH: 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR PRIOR DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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APPLICANT:
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APPLICANT: Cali, Brian
                                                                                                                                                          TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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5. US20020128250A1
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Maxon, Mary
Milne, Todd
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Holtzman, Doug
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                                                             Conservative
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                                                                                  100.0%;
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100.0%; Fred. No.
                                                                                                   80.0%;
                                                             0; Mismatches
                                                                                Score 40; DB 16;
Pred. No. 2.5e+02;
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US-10-425-114-53903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53903
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53903, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                           SEQ ID NO 56925
LENGTH: 260
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                                                                         Matches
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                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                 APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT APPLICATION UNMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                   OTHER INFORMATION: Clone ID: UC-ZMFLMO17086H05_FLI.per
                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                      FEATURE:
                                                                                           Local
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207 NGNGSNG 213
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                                   1 NGNGANG 7
                                                                      Similarity 6; Conserv
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Kovalic, David K
Screen, Steven E
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                                                                         Conservative
                                                                                             74.0%;
85.7%;
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85.7%;
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                                                                         1; Mismatches
                                                                                         Score 37; DB 12; Length 260; Pred. No. 2e+02;
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Pred. No. 1.5e+02;
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RESULT 6

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RESULT 8
US-10-424-599-150886
; Sequence 150886, Application US/10424599
; Publication No. US20040031072A1
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Best Local Similarity
Triches 7; Conserve
                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96690C.1.pep US-10-437-963-201301
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Best Local Similarity
Matches 6; Conserva
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US-10-425-114-44021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 201301, Application US/10437963 ; Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 380
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 201301
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221)B
                                                                                                                                                                                                                                                                                       LENGTH: 452
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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70.0%;
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85.7%;
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1; Mismatches
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RESULT 10
US-10-282-122A-43827
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                                GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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SEQ ID NO 150886
                                                                                                              Sequence 43827, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
LENGTH: 568
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Best Local
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
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CURRENT APPLICATION NUMBER: US/10/086,510
CURRENT FILING DATE: 2002-02-27
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEARL
TITLE OF INVENTION: OYSTER CULTIVATION
APPLICANT:
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APPLICANT: Kovalic David
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LOCATION: (1)..(482)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: Clone ID:
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TYPE: PRT
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                 y Match 74.0%;
Local Similarity 85.7%;
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                  Haselbeck, Robert
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Pred. No. 3.8e+02;
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Zyskind, Judith Ohlsen, Kari

Wall, Daniel

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JS-10-282-122A-43827
                                                APPLICANT: Weko, J.
APPLICANT: Patterson, R.W.
APPLICANT: Patterson, R.W.
TITLE OF INVENTION: Identification of chromosome inheritance modifiers in Drosophila TITLE OF INVENTION: melanogaster
FILE REFERENCE: 1211.015US1
CURRENT APPLICATION NUMBER: US/09/949,029
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/231,178
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 70
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Karpen, G.H.
APPLICANT: Dobie, K.W.
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43827
LENGTH: 1038
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APPLICANT:
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PRIOR FILING DATE: 2000-03-21
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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LENGTH: 296
TYPE: PRT
ORGANISM: Drosophila melanogaster
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APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/253,625
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60.0%;
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; OTHER INFORMATION: Clone ID: 701013187_FLI.pep
US-10-425-114-44598
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SEQ ID NO 7653
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 44598
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Matches 6; Conserv
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                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8000
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                            FILE REFERENCE: 10182-005-999
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/032,585
                                                                                                                                                   TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 376
TYPE: PRT
ORGANISM: Glycine
                                                                                                                                                                                       LENGTH: 420
                                                                                   Local
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 189 NGGGANGE 196
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                                 1 NGNGANGQ 8
                                                                   Similarity 6; Conserv
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yihua
                                                                                   72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
75.0%;
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Pred. No. 3.4e+02;
0; Mismatches 1
                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 12;
Pred. No. 4.3e+02;
1; Mismatches 1
                                                                                     Pred. No. 4.8e+02;
                                                                                                     Score 36; DB 14;
                                                                                                     Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 376;
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JS 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12117
LENGTH: 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-10-156-761-12117
; Sequence 12117, Application US/10156761
; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102737C.1.pep
US-10-424-599-145867
                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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US-10-424-599-145867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145867, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)...(572)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 572
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                      72.0%;
Local Similarity 85.7%;
les 6; Conservation
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744 NGNGGNG 750
                                         1 NGNGANG 7
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Similarity 75.0%;
6; Conservative
                                                                                 0;

    Mismatches

                                                                               Score 36; DB 14; Length 76 Pred. No. 8.9e+02; 0; Mismatches 1; Indels
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                                                                                                                      DB 14; Length 763;
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Search completed: July 21, 2004, 17:17:49 Job time : 2.73448 secs

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Post-processing: Minimum Match 0%
Maximum Match 100
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Maximum DB
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50
                                PIR 78:*
1: pir1:*
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                                                                                                                                                                                                                               283366 seqs,
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                                                                                 Listing first 45 summaries
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pir2:*
pir3:*
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1497.381 Million cell updat
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                                                                                                                                                                                                                                                                                                                                                                            cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

No.	Score	당각	Length	DB.	-	Description
,	σι	0	630	2	JQ1670	polygalacturonase
N	42		539	N	7126	othetical pro
ω	40		534	N	6257	l prot
4	40		979	N	3979	act
ហ	39	8	137	N	80	hypothetical glyci
6	39	78.0	449	N	A24993	ω, 2
7	37		568	N	JC7210	lluscan shell m
80	37	74.0	694	N	AG2353	nslation elo
9	37	74.0	1038	N	H90053	hypothetical prote
10	37	74.0	1519	N	S41525	
11	36	72.0	65	N	I36850	A26L protein - var
12	36	72.0	65	N	T28568	hypothetical prote
13	36		101	N	H72166	
14	36	72.0	175	N	S32957	hypothetical prote
15	36	72.0	253	N	F89030	Ë
16	36	72.0	253	N	T37247	Ca
17	36	72.0	288	۳	GNBPT4	protein
18	36		491	N	D97037	.cal prot
19	36	72.0	673	N	T36717	seri
20	36		693	N	G71302	tpr
21	36	72.0	774	N	T49573	probable ATP-bindi
22	36	72.0	1284	ш	WMVZAI	ıclus
23	36	72.0	1538	N	H70846	Ë.
24	36	72.0	2248	Н	D42088	adenylate cyclase
25	35		219	N	T34523	hypothetical prote
26	35		262	N	T22489	Ë
27	35	70.0	363	N	C97298	7
28	35	70.0	411	N	B97367	μ.
29	35	70.0	411	N	AC2585	pothe

R; Praser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A; Reference number: A71250; MUID:98332770; PMID:9665876
A; Accession: D71260

the syphilis spirochete

거 교 Gwin McDo

hypothetical protein TP0969 - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Ull-1998 #sequence\_revision 24-Ull-1998 #text\_change 05-Nov-1999 C;Accession: D71260

A; Molecule type: DNA A; Residues: 1-539 < COL>

A;Cross-references: GB:AE001264; GB:AE000520; NID:g3323278; PIDN:AAC65927.1; PID:g332329

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30
34	34	34	34	34	3 5	35	35	ω ω	3	ω 5	3 5	35	ω U	<u>د</u> 5	35
68.0	68.0	68.0	68.0	68.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0
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ь	N	Н	N	N	N	Ŋ	N	N	N	N	N	N	N	N	И
Z3BPFD	G84526	G64058	F70787	G82723	T18312	AH1906	T22318	T22488	F71418	S54547	C89451	T49181	D70878	T22835	S48859
coat protein A pre	hypothetical prote	UDP-N-acetylmurama	hypothetical glyci	partition protein	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	PAM1 protein - yea	protein T04G9.6 [i	cyclophylin-like p	hypothetical glyci	hypothetical prote	nucleoside triphos

#### ALIGNMENTS

polygalacturonase (EC 3.2.1.15) 1 beta chain precursor - tomato C;Species: Lycopersicon esculentum (tomato) C;Date: 10-Jun-1993 #secuence revision 10-Jun-1993 #text\_change 21-Jul-2000 C;Date: 10-Jun-1993 #secuence revision 10-Jun-1993 #text\_change 21-Jul-2000 C;Date: Total Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | Polymers | P

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A;Molecule type: protein
A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 109-119;160-171,230-236;243-251;291-293 <ZHE1>
A;Residues: 109-119;160-171,230-236;243-251;291-293 <ZHE1>
A;Experimental source: fruit, cv. Ailsa Craig
A;Experimental source: fruit, cv. Ailsa Craig
C;Comment: This enzyme is a cell wall protein that hydrolyzes pectins.
C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-30/Domain: signal sequence #status predicted <FRO>
F;109-387/Product: polygalacturonase 1 beta chain #status experimental <MAT'>
F;199-387/Product: polygalacturonase 1 beta chain #status predicted <CTP>
F;199-630/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;124,142,256,334,369,387/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                       Ş
                                                                                       Query Match
Best Local Similarity
Watches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
A;Accession: PQ0447
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A; Residues: 1-630 < ZHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: JQ1670; PQ0447
R;Zheng, L.; Heupel, R.C.; DeliaPenna, D.
Plant Cell 4, 1147-1156, 1992
A;Title: The beta subunit of tomato fruit polygalacturonase isoenzyme 1: isolation, A;Reference number: JQ1670; MUID:93005745; PMID:1392611
A;Accession: JQ1670
   243
NGNGANGEFV 252
                                                       NGNGANGOXV 10
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:M98466; NID:g170479; PIDN:AAA34181.1; PID:g170480
                                                                                                                                                     90.0%;
                                                                                                                                              Score 45; DB 2;
Pred. No. 1.8;
                                                                                                                        Mismatches
                                                                                                                        1;
                                                                                                                                                                            Length 630;
                                                                                                                        Indels
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C;Genetics:
A;Gene: SPAC30D11.14
A;Map position: 1L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
S62572
                                                                        A;Cross-references: EMBL:X74152; NID:g450363; PIDN:CAA52267.1; A;Experimental source: strain $288C R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; submitted to the Protein Sequence Database, March 1994 A;Reference number: $37825
                                                                                                                                                                                                                                                                                                                                                                                                        R;Marczak, J.E.; Brandriss, M.C.
MOl. Cell. Biol. 11, 2609-2619, 1991
A;Title: Analysis of constitutive and noninducible mutations
A;Reference number: A39792; MUID:91203881; PMID:2017167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: protein YKL015w
C;Species: Saccharomyces cervisiae
C;Date: 07-Feb-1992 #sequence revision 07-Feb-1992 #text_change
C;Accession: A39792; S34701; S37828; S37832; S16705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain Nichol C; Genetics:
A; Cross-references:
A; Experimental source
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-979 <WIE>
                                                                                                                                                                                                                                 A;Description: Sequencing and analysis of 51.5 kilobases A;Reference number: S34679
A;Accession: S34701
                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X55384; NID:g4251; PIDN:CAA39055.1; PID:g4252 R;Wieman, S.; Voss, H.; Schwagaer, C.; Rupp, T.; Stegemann, J.; Zimmu submitted to the EMBL Data Library, July 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
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A; Accession: T38585
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                                      A;Residues:
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A;Residues: 1-979 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-534 <PE2>
                                                          A; Molecule type: DNA
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                                      1-979 <WI2>
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8; Conser
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source:
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  EMBL:Z28015; NID:g486002;
ce: strain S288C
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                  PID:g486003; MIPS:YKL015v
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70811
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ht.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Skelton, S.; Squares, S.;
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F;34-60/Region: zinc finger
                                                                                                                                                                                                                                                                                                               RESULT
A24993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-137 < COL>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical glycine-rich protein Rv0832 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis (C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
A;Molecule type: DNA
A;Residues: 1-449 <WON>
A;Cross-references: GB:M15823; NID:g144409; PIDN:AAA23084.1; PID:g144410
A;Note: the amino-terminal sequence of the mature protein (residues 32-6)
                                                                                                               A; Title: Characterization and structure of A; Reference number: A24993; MUID:87055249;
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A; Residues: 1-825 < RIE>
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                                                                                           A; Accession: A24993
                                                                                                                                                        Gene 44, 315-324, 1986
                                                                                                                                                                               R; Wong, W.K.R.; Gerhard, B.; Guo,
                                                                                                                                                                                                      C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Mar-2000
C;Accession: A24993
                                                                                                                                                                                                                                             C; Species: Cellulomonas fimi
                                                                                                                                                                                                                                                                      N;Alternate names: endo-1,
                                                                                                                                                                                                                                                                                        cellulase (EC 3.2.1.4) precursor -
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Experimental source: strain S288C
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Pred. No.
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Pred. No.
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C; Genetics:
A; Gene: cenA
C; Function:
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Nakazaki, N.; Shimpo, S.; Sugımoto, m.; Aumunum.
DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Title: Complete Genomic Sequence of the Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamentous Nitrogen Filamento
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-201 #sequence_revision 14-Dec-2001 #text_change
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                                                                                                                                                                                                                  A;Cross-references: GB:BA000019; PIDN:BAB76082.1; PID:g17133519; GSPDB:GN00179 A;Experimental source: strain PCC 7120
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Biochem. Biophys. Res. Commun. 269, 213-218, 2000
Biochem. Biophys. Res. Commun. 269, 213-218, 2000
A;Title: Wolecular mechanism of the nacreous layer formation
A;Reference number: JC7210; MUID:20160475; PMID:10694502
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A; Residues: 1-568 < KON>
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85.7%;
                                                        74.0%;
85.7%;
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75.0%;
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Pred. No.
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Pred. No.
                                     Pred. No. 58;
l; Mismatches
                                                                                   Score 37;
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16;
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58;
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                                                                                                                                       translation elongation
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                                     0;
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                                     Indels
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09-Dec-2002
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                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe, A.; ; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų.
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A; Accession: S77974
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A; Residues: 1-1519 < OTO>
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Matches
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70.0%;
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Pred. No.
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C;Species: Helicobacter mustelae

C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997

C;Accession: S41525; S77974

R;O'Toole, P.W.; Austin, J.W.; Trust, T.J.

Mol. Microbiol. 11, 349-361, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; McGessaum.
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1038 < KUR>
A; Residues: 1-1038 < KUR>
A; Cross-references: GB:BA000018; PID:g13702453; PIDN:BAB43594.1; GSPDB:GN00149
A; Cross-references: Strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H90053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus (c;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: H90053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major ring-forming surface protein precursor - Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
Izutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
a, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                    molecular characterization of a MUID:94224153; PMID:8170397
                                                                                                                                                                                                                                                                                                NID:g431303; PIDN:AAC36865.1; PID:g431304
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          Mismatches
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88;
3e+02;
3;
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                                                      Length 1519;
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                                                                                                            #status experimental <MAT>
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#text\_change

23-Mar-2001

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R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28568
                                                                                                                                               A;Experimental source: strain Garcia-1966
C;Genetics:
                                                                                                                                                                                                                                                               R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola A;Reference number: A72150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein A27L - variola major virus C;Species: variola major virus C;Species: variola major virus C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000 C;Accession: T28568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49071.1; PID:g457021
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                                                                                                                                                                                                                                                                                                                                                                                  A27L protein - variola minor virus (strain Garcia-1966)
                                                                                                                                                                                                Status: preliminary
Molecule type: DNA
Residues: 1-101 <SHC>
                                                                                                                                                                                                                                                                                                                                                 Species: variola minor virus
Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
                                                                              Query Match
Best Local
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57
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6; Conserv
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Pred. No. 7.
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RESULT 14

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R; anonymous, The C. elegans Sequencing Consortium.

R; anonymous, The C. elegans Sequencing Consortium.

R; anonymous, The C. elegans Sequence 282, 2012-2018, 1998

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A; Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/

A; Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
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Yeast 9, 189-199, 1993
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A;Reference number: S29348; MUID:93220397; PMID:8465606
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
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RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
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RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
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87.5%;
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ota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                       B38F20B8A20A47F7 CRC64;
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TRANSFAC; T01163; -.
TRANSFAC; T01163; -.
SGD; S0001498; PUT3.
GG; GO:0005634; C:nucleus; IC.
GG; GO:0003704; F:specific RNA polymerase II transcription fa.
GG; GO:0003704; P:positive regulation of transcription from P.
GG; GO:0045944; P:proline catabolism; IMP.
InterPro; IPR0071219; Fungal_trans.
InterPro; IPR007138; Fungi_TrN.
                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 31-100.
MEDLINE=97448679; PubMed=9303004;
Swaminathan K., Flynn P., Reece R.J., Marmorstein R.;
"Crystal structure of a PUT3-DNA complex reveals a novel mechanifor DNA recognition by a protein containing a Zn2Cys6 binuclear
                                                                                                                                                                          GermOnline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walters K.J., Dayle K.T., Reece R.J. "Structure and mobility of the PUT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97448678; PubMed=9303003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 30-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequencing and analysis of 51.6 kilobases on the left arm of chromosome XI from Saccharomyces cerevisiae reveals 23 open reframes including the FASI gene.";
Yeast 9:1343-1348(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marczak J.E., Brandriss M.C.; "Analysis of constitutive and noninducible mutations of transcriptional activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last annotatic Proline utilization trans-activator. PUT3 OR YKL015W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94205264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=91203881; PubMed=2017167;
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                                                                                                                                    BL; X55384; CAA39055.1; -
BL; X74152; CAA52267.1; -
BL; Z28015; CAA81850.1; -
R; A39792; A39792.
B; 1AJY; 17-SEP-97.
B; 1AJY; 17-SEP-98.
B; 1ZMB; 16-SEP-98.
TMODLINE; 139771; -
ANSERC; T01163; -
D; S0001498; PUT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: POSITIVE ACTIVATOR OF THE PROLINE UTI BLINDS TO THE PROMOTERS OF PUT1 AND PUT2 GENES. BINDS TO THE DNA SEQUENCE 5'-CGG-N(10)-CCG-3'. SUBCUNIT: Binds DNA as a homodimer. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type SIMILARITY: Contains 1 Zn(2)-Cys(6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Struct. Biol. 4:751-759(1997). FUNCTION: POSITIVE ACTIVATOR OF
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H., Schwager C., Rupp
othues D., Sensen C.,
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Erfle H., Hewitt
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase 1 precursor (BC 3.2.1.4) (Endo-1,4-beta-glucanase (Cellulase I) (CMCASE I) (CEL1).
                                                                                     between
the Euro
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PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.

PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.

Transcription regulation; Activator; DNA-binding; Nuclear Zinc; Metal-binding; Proline metabolism; 3D-structure.

ZNC2_CYS(6), FUNGAL_TYPE.
                                                                                                                                                                                                                                                                                                            MEDLINE=93015685; PubMed=1400190; Fernandez-Abalos J.M., Sanchez P., Col Villanueva J.R., Perez P., Santamaria "Cloning and nucleotide sequence of ce endo-beta-1,4-glucanase-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00172; Zn clus;
PRINTS; PR00054; FUNGAL;
SMART; SM00066; GAL4; 1
                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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STRAIN=JM8 / CECT3310;
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                                                                                                                                                                                                          ACTIVITY: En
in cellulose,
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                                  http://www.isb-sib.
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(family 6 of gly
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                                                                                                                                 Gilkes N.R., Claeyssens M., Aebersold R., Henrissat B., Morrison H.D., Kilburn D.G., Warren R.A.J., Miller R.C. "Structural and functional relationships in two families
                                                                                                                                                                                                            Gilkes N.R., Kilburn
"Structural and funct
proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003733; Glyco_hydro_6; 1.
PROSITE; PS00655; GLYCOSYL_HYDROL_F6_2;
PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2;
                                                                                                                                                                                                                         MEDLINE=90036847; PubMed=2681184; Gilkes N.R., Kilburn D.G., Miller R. "Structural and functional analysis
                                                                                                                                                                                                                                                                                           "Characterization and structure Cellulomonas fimi.";
                                                                                                                                                                                                                                                                                                                   Wong W.K.R.,
Miller R.C.
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Micrococcineae; Cellulomor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00733; GLHYDRLASE6
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HSSP; P26222;
                                                                                                                      glycanases."
                                                                                                                                                                                                                                                                                 Gene 44:315-324(1986).
                                                                                                                                                                                                                                                                                                                                                                                                           Cellulomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoglucanase A precursor
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                                                                                                                                                                     MEDLINE=92104156; PubMed=1761039;
                                                                                                                                                                                 DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                (Cellulase).
                                                                                                                                                                                                      Biol.
        PUNCTION: The biological conversion of cellulose to glucose generally requires three types of hydrolytic enzymes: (1) Endoglucanases which cut internal beta-1,4-glucosidic bonds; Exocellobiohydrolases that cut the dissaccharide cellobiose from the nonreducing end of the cellulose polymer chain; (3) Beta-1,4-glucosidases which hydrolyze the cellobiose and othe short cello-oligosaccharides to glucose.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucoans.
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PF01341; Glyco_hydro_6; 1.
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                                                                                                              Biochem. 202:367-377(1991).
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linker region
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                                                                                                                                                                                                     264:17802-17808(1989).
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t annotation u
(EC 3.2.1.4)
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BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
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 cereal beta-D-glucans. "hinge") may be a pote
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cellulase
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Pfam; pF00553; CBM_2; 1.

Pfam; pF00553; CBM_2; 1.

Pfam; pF01341; Glyco_hydro_6; 1.

PRINTS; pR00733; Glyco_hydro_6; 1.

PRODom; p0003733; Glyco_hydro_6; 1.

SMART; SM00637; CBD_II; 1.

PROSITE; pS00665; GLYCOSYL_HYDROL_F6_1; 1.

PROSITE; pS00656; GLYCOSYL_HYDROL_F6_2; 1.

R PROSITE; pS00656; GLYCOSYL_HYDROL_F6_2; 1.

R PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
 "The complete sequence of a 19,482 bp segment arm of chromosome II from Saccharomyces cerev Yeast 9:189-199(1993).
                                                                                                                                                                               TR20_YEAST STANDARD; PRT; 175 AA.
1938334;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-200 (Rel. 41, Last annotation update)
Transport protein particle 20 kDa subunit (TRAPP TRS20 OR YER254C OR YER1722.
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ACT_SITE
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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InterPro; IPR008965; Cellul_bind.
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by non-profit institutions as long as its content
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SIMILARITY: Belongs to cellulase family B (family 6 of glycos hydrolases).
SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
                                                                                                                             TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain.
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CELLUICSE-BINDING.
LINKER ("HINGE") (PRO-THR BOX)
CATALYTIC.
BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39;
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                                          segment located
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                             cerevisiae.";
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Matches
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01-JUL-1989
01-JUL-1989
10-OCT-2003
                                                                                                                                                                                                  Nucleic
[2]
                                                                                                                                                                                                                  MEDLINE=89263746; PubMed=2726468; Prilipov A.G., Selivanov N.A., Efimov V Wesyanzhinov V.V., Mesyanzhinov V.V., "Nucleotide sequences of bacteriophage "Nucleic Acids Res. 17:3303-3303(1989).
                                                                      Miller E.S., Kutter E., Mosig G., "Bacteriophage T4 genome."; Microbiol. Mol. Biol. Rev. 67:86-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BPT4
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMEDLINE=20015372; PubMed=10545330;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T4
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Transport; Endoplasmic reticulum; Golgi stack.
SEQUENCE 175 AA; 19700 MW; 82285CAEAC2735D9
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EMBL; Z36123; CAA85217.1;
PIR; S32957; S32957.
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                                                                                                                                                MEDLINE=22514363; PubMed=12626685;
                                                                                                                                                                      SEQUENCE FROM N
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GO; GO:0006888; P:ER to Golgi transport; IMP.
GO; IPR006732; Sedlin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD;
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reticulum to Golgi traffic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Online; 138797; -. $0000458; TRS20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%;
85.7%;
                                                                           Rev. 67:86-156(2003).
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0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stage; Caudovirales; Myoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Baseplate wedge protein
                                                                                                                      Arisaka F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex on the cis-Golgi that
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                                                                                                                                                                                                                                                                                        V.P., Marusich
                                                                                                                                                                                                                                                T4
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                                                                                                                         Kunisawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burston J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                      Ruger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kostyuchenko V.A., Navruzbekov G.A., Kurochkina L.P., Mesyanzhinov V.V., Rossmann M.G.; "The structure of bacteriophage T4 gene product 9: the
                                                                                             TURN
                                                                                                                     TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X14192; CAA32395.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structure 7:1213-1222(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tail contraction."
                                                                                   STRAND
                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                                                                        Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Structural component of the baseplate. Connects the long tail fibers to the baseplate and triggers the tail contraction after virus attachment to a host cell.
                                                                                                                                                                                                                                                                                                                                                                                                          S04082;
                                                                                                                                                                                                                                                                                                                                                                                                                          AF158101; AAD42520.1; -.
Б
2
                μ
                                Similarity 6; Conserv
NGTGADGQII 61
                 NGNGANGOXV 10
                                                                                                                                                                                                                                                                                                                                                                                                  IPR008987; Gp9
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                                                                   288
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   GNBPT4.
                                                                  AA;
                                                                                           166
180
184
193
196
208
210
224
228
239
259
                                                                 282
30997 MW;
                                                                                                                                                                                                                         3D-structure
                                         72.0%;
60.0%;
                                         Score 36; DB
Pred. No. 18;
                                                                   8028FCEBA25BB760 CRC64;
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                 DB 1;
                                                 Length 288;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strelkov S.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trigger for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . a collaboration
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RESULT 8
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Q9XA16;
10-OCT-2003
                                                                                                                         DOMAIN
DOMAIN
NP BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 417:141-147(2002).

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phospho
-i- CATALYTIC ACTIVITY: ATP + a protein family of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quali M.A., Kieser H., Harris D.E., Quali M.A., Kieser H., Collins M., Eromin A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1:

Hypothetical protein; Transferase; Serine/threonine-protein kinase;

Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                            EMBL; AL939118; CAB45215.1; -.
plr; T36717; T36717.
InterPro; IPR005243; PASTA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; NCBI_TaxID=1902; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable serine/threonine-protein SCO3848 OR SCH69.18.
                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00740; PASTA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine/threonine-protein kinase SCO3848
                                                                                                                                                                                                                                                                                                                                   Pfam; PF03793; PASTA; 4. Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the Ser/Thr far-
-!- SIMILARITY: Contains 4 PASTA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                          SEQUENCE
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                         DOMAIN
 654
                                                   Similarity 6; Conserv
 NGNGGNG
                          NGNGANG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacteria; Actinobacteridae; Actinomycetales; cineae; Streptomycetaceae; Streptomyces.
                                                                                                                                      379
446
512
581
17
40
                                                     Conservative
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                                                                                                           AA;
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 660
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511
580
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138
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85.7%;
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PASTA 2.
PASTA 3.
PASTA 4.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                Score 36;
                                                                   Pred. No.
                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                       proteome.
PROTEIN KINASE.
                                                                                                           42A0615E239722DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioinformatics
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce,
                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã
                                                                                1; Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprotein.
protein kinases.
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RESULT 10
CYA1_DROME
ID CYA1_DROME
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Matches
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P16602;
01-AUG-1990 (Rel.
01-AUG-1990 (Rel.
01-NOV-1990 (Rel.
A-type inclusion E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COWPX
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REPEAT
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REPEAT
                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                    EMBL; D00319; BAA00222.1; -.
                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patel D.D., Pickup D.J.; "Messenger RNAs of a strongly-expressed late gene of cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88111568; PubMed=2828037;
Patel D.D., Pickup D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Funahashi S., Sato T., Shida H.; "Cloning and characterization of the gene encoding the major protein of the A-type inclusion body of cowpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
Orthopoxvirus.
                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                    Late protein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-109 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88089536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CPRO6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cowpox virus (CPV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Virol. 69:35-47(1988).
                                                           1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                        O J. 6:3787-3794 (1987).

FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO BEEN ASSUMED THAT SUCH BODIES PROTECT THE V DISSEMINATION FROM ANIMAL TO ANIMAL.

MISCELLANEOUS: A CHARACTERISTIC FEATURE OF LARGE MASSES WITH NO SURROUNDING MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFECTED CELLS.
                                                                                                                                                                                                                                                                                                               ; X06343; CAA29650.1; -. JQ0006; WMVZAI.
                                                                                                                                                                                                                                                                                         PF04508; Pox_A
                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5'-terminal poly(A)
                                                           NGNGGNG
                                                                               NGNGANG 7
                                                                                                                                                                                                                                                                                                   IPR007596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 15, (Rel. 16,
                                                                                                      Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                AA;
                                                          1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein (ATI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=2826668;
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                                                                                                                                                                      912
637
665
689
720
751
780
811
842
871
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\_type_inc;
                                                                                                               72.0%;
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Last annotation update)
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                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences.";
                                                                                                               Score 36;
Pred. No.
                                                                                                                                                                                                                                                                    10 X
   PRT;
                                                                                                    Mismatches
                                                                                                                                               F7904C9E1DE8D012 CRC64;
                                                                                                                                                                                                                                                                     APPROXIMATE
   2248 AA
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                                                                                                               DB
89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE VIRUS
                                                                                                                        ۲.
                                                                                                                                                                                                                                                                   TANDEM REPEATS
                                                                                                                        Length 1284;
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                                                                                                    Indels
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JS DURING
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CAMP biosynthesis; Lyase; CalmouuL,

Marnesium; Repeat; Transmembrane; Glycoprotei

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01-OCT-1993
15-MAR-2004
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PROSITE; PS00452; GUANYLATE CYCLASES 1;

PROSITE; PS50125; GUANYLATE CYCLASES 2;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00211; guanylate_cyc;
SMART; SM00044; CYCc; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P19754; 1AWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; D42088; D42088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M81887; AAA28844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ca2+/Calmodulin-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed R.R.;
"The Drosophila learning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92154664; PubMed=1739965;
Levin L.R., Han P.-L., Hwang P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0019933; P:CAMP-mediated signaling; NAS. GO:0007625; P:grooming behavior; NAS. GO:0007591; P:molting cycle (sensu Insecta) GO:000855; P:olfactory learning; NAS. GO:0045473; P:response to ethanol (sensu Insert); IPR001054; G.cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate. COFACTOR: Binds 2 magnesium ions per subunit (By similarity). ENZYME REGULATION: Activated by calcium/calmodulin and G protein. SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Mushroom bodies of the fly brain.
DOMAIN: Composed of two homologous domains.
SIMILARRITY: Belongs to the adenylyl cyclase class-4/guanylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 memory defect.
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(Rel. 27, Last sequence update)
(Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                TE_CYCLASES_1; 2.
TE_CYCLASES_2; 2.
Calmodulin-binding; Metal-binding;
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cyclase.";
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era; Muscomorpha;
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                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (see http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidyl-prolyl (Cyclophilin) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGEN
                                       EMBL; U81792; AAB39880.1; HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of in planta-induced rust genes haustorium-specific cDNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97294919; Pu Hahn M., Mendgen K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=55588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Basidion 
Uredinales; Pucciniaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                  its effects via an inhibitory action on PPTase SUBCELLULAR LOCATION: Cytoplasmic (By similarity) DEVELOPMENTAL STAGE: Haustoria and rust-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                         . Plant Microbe Interact. 10:427-437(1997). FUNCTION: PPTases accelerate the folding of proteins. the cis-trans isomerization of proline imidic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1269
                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the cyclophilin-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                               oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega=180)
                                                                                                                                                                                                                                                                                 observed, in lower levels,
                                                                                                                                                                                                                                                                                                                                                            ENZYME REGULATION: Binds cyclosporin
                                                                                                                                                                                                                                                                                                                                                                                   (omega=0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UROFA
Pro; IPR002130; CSA_PPIase.
PF00160; pro_isomerase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 38, Createu)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)
olyl cis-trans isomerase (EC 5.2.1.
olyl cis-trans isomerase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rust fungus).

ji; Basidiomycota; Urediniomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2241
280
281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334
1029
530
602
1297
1297
1810
2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9150592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324
800
807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC CATALYTIC GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
G->R: ABOLISHES CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
MAGNESIUM 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGNESIUM 1
MAGNESIUM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLY/SER-RICH
ASP/GLU-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                 in spores or hyphae formed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E459C718BE018868 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND 2 (BY SIMI
(VIA CARBONYL
                                                                                                                                                                                                                                                                                                                                                              A (CSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ACIDIC).
                                                                                                                  http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Planta-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8) (PPIase) (Rotamase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urediniomycetidae;
                                                                                                                                                                                                                                                                                                                                                                CSA mediates some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
DNYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                        П
                                                                                                                                                                                                                                                                                                      leaves. Also
                                                                                                                                                                                                                                                                                                                                                                                                      peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY
                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                             It catalyzes bonds in
                                                                                                                                                                                                                                                                                 п
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                      for
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                                                                                                                                                                                                                                                                                 vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rust
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
NIPL_MO
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Best Local
                                                Matches
                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00153; CSAPPISMRASE.
PROSTIE; PS00170; CSA PPIASE]; 1.
PROSTIE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family.
Cyclosporin; Isomerase; Rotamase; Moda641CBA0DBD1D CRC64;
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99084982; PubMed=9867803; Chen G., Cizeau J., Vande Velde C., Shi L., Dubik D., Greenberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.-MAY-2000 (Rel. 39, Created)
30.-MAY-2000 (Rel. 39, Last sequence update)
15.-MAR-2004 (Rel. 43, Last annotation update)
BCL2/adenovirus E1B 19-kDa protein-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NIP3-like protein X).
BNIP3L OR NIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Z2F7;
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                               Apoptosis;
TRANSMEM
                                                                                                                                     MGD; MGI:1332659; Bnip31.
                                                                                                                                                    EMBL;
                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nix and Nip3 form a subfamily of pro-apoptotic
                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSUE=Embryo;
                                                                                                                                                                           send
                                                                                                                                                                                                                                                                                                        SÜBÜNIT: Homodimer (Probable).
SUBCELLULAR LOCATION: Mitochondrial.
PTM: Undergoes progressive proteolys
fragment, which is blocked by the p
                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 274:7-10(1999).

FUNCTION: Induces applicates. Interacts with viral and anti-apoptosis proteins. Can overcome the suppressers BCL-XL, although high levels of BCL-XL expression will anoptosis. May function as a tumor suppressor.
                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                            lactacystin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
48
                                                                                                                                                    AF067395; AAD03588.1; -.
                                               Similarity
6; Conserv
                                                                                                                                                                           s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGNGANGQXV 10
                         NGNGANG
                                                                                                               Transmembrane; Mitochondrion.
187 207 POTENTIAL.
                                                                                                 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                             Belongs to the NIP3 family.
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4
                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
50.0%;
                                                                                                   23766
                                                            70.0%;
85.7%;
                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                0;
                                                  Pred. No. 21;
0; Mismatches
                                                                        Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                     proteolysis to an by the proteasome
                                                                                                 EAA839DEFDDE50D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                            No.
                                                                                                                                                                                                                                                                                                                                                                       BCL-XL expression will inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park J.H., Bozek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
15;
                                                              21;
                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                          1.
                                                                                                                                                                                                                                                                                                                      an 11 kDa C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                          Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial
                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                          inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                   Indels
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                                                                                                                                                                                                                              restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 like (NIP3L)
                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolton
                                                                                                                                                                                                                                                                                                                                                                                  BCL-2
                                                                                                                                                                                                                                                                                                                                                                                               cellular
                                                                                                                                                                                                                                                        a collaboration
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HUMAN

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helfon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Chenerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Dermal papilla;
Faroog M., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Sohn M. Faroog M., Chung H.J., Im S.U., Jung E.J., Kim J.C.;
"A catalog of genes in the human dermal papilla cells as expressed sequence tags.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99084982; PubMed=9867803;
Chen G., Cizeau J., Vande Velde C
Shi L., Dubik D., Greenberg A.;
"Nix and Nip3 form a subfamily of
proteins.";
                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsujimoto Y., Suzumori K., Nakamura Y., "Isolation, mapping, and functional analysis of (BNIP3I) enroding a protein homologous to human Genes Chromosomes Cancer 21:230-235(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JMAR-2004 (Rel. 43, Last annotation update)
BCL2/adenovirus EIB 19-kDa protein-interacting protein 3 like (NIP3L)
(NIP3-like protein X) (BCL2/adenovirus EIB 19-kDa protein interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIPL_HUMAN
060238;
                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasuda M., Han J.-W., Dic
"BNIP3a, a human homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein 3A).
BNIP3L OR BNIP3A OR NIX OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsushima M., Fujiwara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98183799; PubMed=9523198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                                                                                                                                                                  (NOV-2001)
                                                                                                                                                                                                                                                                                                                                                            marrow,
                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274:7-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                          ", and Cervix;
PubMed=12477932;
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H
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log of pro-ap
                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with
                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Takahashi E
Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BNIP3H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e C.A., Boyd J.M., Chinnadurai G.;
pro-apoptotic protein BNIP3, promo
h viral and cellular anti-apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro-apoptotic mitochondrial
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Best Local :
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EMBL; AF079221; AAC27723.1; --
EMBL; AF07396; AAD03589.1; --
EMBL; AF255051; AAF70290.1; --
EMBL; AF452711; AAL50978.1; --
EMBL; BC001559; AAH01559.1; --
EMBL; BC009603; AAH09603.1; --
                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
phosphohydrolase) (NTPase) (Apyrase).
                                                                                                                                                                                                                                                                       01-OCT-1996
01-OCT-1996
28-FEB-2003
STRAIN=cv. Alaska; TISSUE=Stem; Shibata K., Abe S., Davies E.; "Structure of the coding region Pisum sativum.";
                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisu
                                                                                                                                                                                                                                                                                                                                         PEA
                                                                                                    STRAIN=cv. Alaska; TISSIE=Plumule; MEDLINE=96197404; PubMed=8616230; Hsieh H., Tong C.G., Thomas C., Roux S"Light-modulated abundance of an mRNA
                                                                             chromatin-associated NTPase in pea."; Plant Mol. Biol. 30:135-147(1996).
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NTPA_PEA
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=3888;
                                                                                                                                                                                                                                    Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                               P52914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005739; C:mitochondrion; TAS.
GO; GO:0006917; P:induction of apoptosis;
GO; GO:0006634; P:negative regulation of s
Apoptosis; Transmembrane; Mitochondrion.
TRANSMEM 188 208 POTENTIAL.
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SIMILARITY: Belongs to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Induces apoptosis. Interacts with viral and cellular anti-apoptosis proteins. Can overcome the suppressers BCL-2 an BCL-XL, although high levels of BCL-XL expression will inhibit
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85.7%;
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Pred. No. 21;
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RESULT 15
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01-OCT-1996
01-OCT-1996
                                                                                                                                                     between the Swiss Institute of Bioinformatithe European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
         Pfam; PF00091; tubulin; 1.
Pfam; PF03953; tubulin C; 1.
PRINTS; PR01161; TUBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TBG
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Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Hydrolase; Nuclear protein.
                                                InterPro; IPR008280; Tub FtsZ C.
InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin_FtsZ.
                                                                                                EMBL; X97250; CAA65885.1;
                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        amoeba Reticulomyxa filosa.";
Eur. J. Cell Biol. 72:287-296
                                                                                                                                                                                                                                                                                                                                                 Nube-Granderath \dot{E}., Schliwa M.; "Unusual distribution of gamma-tubulin in the giant fresh water
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97273248;
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=46433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reticulomyxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Granuloreticulosea; Athalamea; Reticulomyxidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reticulomyxa filosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tubulin gamma chain (Gamma tubulin).
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                SIMILARITY: Belongs to the tubulin family.
                                                                                                                                                                                                                                                           tubulin is found at microtubule organizing centers (MTOC) such the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
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FUNCTION: Might be involved in RNA transport out contaxing ACTIVITY: NTP + H(2)O = NDP + phosphate.
                                                                                                                                                                                                                                                                                                          FUNCTION: Tubulin is the major constituent of microtubules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETFI
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Matches 6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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y Match Local	SEQUENCE		CHAIN	SIGNAL	_	Pfam; PF03	Interpro:	PIR: J01670: J01670.	EMBL: U633	EMBL; M98466; AAA34181.1;	watson C.F., Schuchman B., Liu J., Derrapenna Submitted (Jan-1997) to the EMBL/GenBank/DDBJ	STRAIN=VENT CHERRY;	SEQUENCE FROM N.A	[2]	Plant Cell	features."	isolation,	"The beta	Zheng L., Heupel R.C., Dellapenna	MEDLINE=93005745; PubMed=1392611;	UENCE	Ξ	NCBI_TaxID=4081;	lamiids; Solanales; Solanaceae; Solanum.	Spermatophyta; Magnoliophyta; eudicotyledons;	Eukaryota; Viridiplantae; Streptophyta;	Lycopersicon esculentum (Tomato).	Polygalacturonase iscenzyme	01-JUN-2003	01-NOV-1996	01-NOV-1996		040161	11
similarity	630 AA;		109 3			PF03181; BURP;	InterPro: IPR004873:	0: JO1670.	U63374: AAB39547.1:	66; AAA341	(TAN-1997)	T CHERRY;	ROM N.A.		4:1147-1156(1992)	· ·	characterization,	beta subunit of tomato fruit	Heupel R.C	0057 <b>4</b> 5; Pu	FROM N.A.		=4081;	olanales;	yta; Magno	Viridipla	on esculen	uronase is			6 (TrEMBLrel.	004735	PRELIMINARY:	
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IE
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB dep_Rec; 1.
Receptor; Complete proteome.
SEQUENCE 710 AA; 80884 MW; 9BCFF29D77C
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Virology 275:294-305(2000).
Virology 275:294-305(2000).
EMBL; AF-95902; AAK27935.1;
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MEDLINE=20455575; PubMed=10998330;
Desiere F., Pridmore R.D., Brussow H.;
"Comparative genomics of the late gene cluster from lactobacillus
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Best Local :
SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg (
Delbher A., Utterback T., Weidman J., Khouri H., Gill J., Mikul
Bishai W.;
                                                                                                                                                                                                                                                                                                                                     MEDLINE-9825987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O53843 PRELIMINARY; PRT; 150 AA.
O53843;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PE-family protein (PE_PGRS family protein).
RV0832 OR MT0854 OR MTV043.24.
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MEDLINS=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Parkis B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Corynebacterineae; Mycobacteriaceae;
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PE_PGRS12 OR MB0855.
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Last annotation update)
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Pred. No.
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HSSP; P26222; 17ML.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-c
GO; GO:0005975; P:carbchydrate metabolism; IEA.

InterPro; IPR003305; CBM_CenC.

InterPro; IPR003305; CBM_CenC.

InterPro; IPR001524; Glyco_hydro_6.

Pfam; PF02018; CBM_4_9; 1.

Pfam; PF02018; CBM_4_9; 1.

Pfam; PF020134; Glyco_hydro_6; 1.

PRINTS; PR00733; GLYCO_hydro_6; 1.

PROSITE; P800373; GLYCO_hydro_6; 1.

PROSITE; P800655; GLYCO_NULHYDROL_F6_1; 1.
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Submitted (APR-2001) to the EMBL/Geni
EMBL; ALO22004; CAA17638.1; ALT_INIT.
EMBL; AE006974; AAK45095.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barray S.;
Submitted (FEB-1999) to the
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ProDom; PD001223; PE_region;
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TubercuList; Rv0832;
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59E6472401517B50 CRC64;
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RX MEDLINES—20195066, PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,
RA Dodson K., Doup L.E., Downes M., Dugar-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugar-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugar-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mang T.Y., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Jalaila M., Salussh F., Karpen G.H., Ke Z., Kennison J.A., Weshon D.L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Stapleton M., Strong R., Sun B.,
RA Shue B.C., Stapleton M., Strong R., Sun B.,
Ra Shue B.C., Shen B., Ra Harris M., 
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"An exploration of the sequence of a 2.9-Mb region of the genome Drosophila melanogaster: the Adh region.";
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"The Drosophila beaten path gene encodes a novel secrete
regulates defasciculation at motor axon choice points.";
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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BEAT-IA OR CG4846.
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NCBI TaxID=7227;
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AE003415; AAF449
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01-OCT-2002
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB073680; BAB91157.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004899; F:carbonate debydratase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0007186; P:G-protein compound metabolism; IEA.
GO; GO:0007196; P:one-carbon compound metabolism; IEA.
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Vetigastropoda; Trochoidea; Turbinidae; Turbo
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01-MAR-2002
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InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
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Burkholderiaceae; Ralston:
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GG; GO:005198; F:structural molecule
InterPro; IPR000736; Adeno hexon.
Pfam; PF01065; Adeno hexon; 1.
Pfam; PF03678; Adeno hexon; 1.
ProDom; PD002815; Adeno hexon; 1.
SEQUENCE 913 AA; 102531 MW; 9799F0
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Arch. Virol. 142:1193-1212(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97372953; PubMed=9229008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA vi
NCBI_TaxID=46916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine adenovirus type :
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hexon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reubel G.H., Studdert M.J.;
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1020
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                                                        <u>ا</u>
                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
NGNGAGGRRV 1029
                                                        NGNGANGQXV 10
                                                                                                                                                                                                                                                                  proteome
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                                                                                                                                                                                                                                         1051 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                76.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Betaproteobacteria; Burkholderiales;
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                                                                                                                 Score 38; DB
Pred. No. 3.9e
1; Mismatches
                                                                                                                                                                                                                                         MW;
                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 12;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.40
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
9799FCC746585010 CRC64;
                                                                                                                                                                                                                                         C5E63D3F3DF742B9
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                                                                                                                                                DB 16;
3.9e+02;
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                                                                                                                                                                          Length 1051;
                                                                                                                                                                                                                                         CRC64;
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RESULT 11

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         Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cark R., Caronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Gobbe A., Goodhead I., Gwilliam R., Hamin N., Hance Z.,
A Harper D., Hausser H., Hornsby T., Holroyd S., Horrocks P.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Knights A., Maddison M., Price C., Quail M.A., Rabbinowitsch E.,
A Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Cliver K., Ormond D., Smith R., Squares R., Squares S., Stevens K.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Neture Alas. Spring A., Newbold C., Barrell B.G;
Neture Alas. Scrope S., Smith R., Squares R., Squares R., Squares R.,
Neture Alas. Spring A., Newbold C., Barrell B.G;
Neture Alas. Spring A., Newbold C., Barrell B.G;
Neture Alas. Spring A., Newbold C., Barrell B.G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of a Gibberella fujikuroi (Fu fujikuroi) NAD-dependent glutamade dehydrogenase gene.";

Submitted (Febr-2001) to the EMEL/GenBank/DDBJ databases.

R EMBL; AJ310444; CAC27837.1; -.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

RGO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0006520; F:amino acid metabolism; IEA.

R InterPro; IPR006095; GLFV dehydrog.

R InterPro; IPR006095; GLFV dehydrog.

R InterPro; IPR006096; GLFV_dehydrog_N.

R Ffam; FF00209; GLFV_dehydrog; 1.

Pfam; PF02812; GLFV_dehydrog_N; 1.

Pfam; PF02812; GLFV_dehydrog_N; 1.

RROSSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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01-MAR-2003
01-OCT-2003
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Q81220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22255708; PubMed=12368867;
Hall N., Pain A., Berriman M., Chu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum 
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Hypocreomycetidae; Hypocreales;
NCBI_TaxID=5127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibberella fujikuroi (Bakanae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9C2U8;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TremBLrel. 17, Created)
(TremBLrel. 17, Last sequence up
(TremBLrel. 24, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexa;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 3; Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C79B4061C066DDD7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2646 AA
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Q7T137;
01-OCT-2003
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SI:bZ1G18.3
                                                        SEQUENCE
Briggs S.
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Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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01~DEC-2001
Devoto A., Haramino G.,
                                      Submitted
                                               Briggs S.P., !
"Manipulation
                                                                                            Spermatophyta; Magnoliophyta; PACCAD clade; Panicoideae; And
                                                                                                                         Zea mays (Maize)
                                                                                                                                 Seven transmembrane protein
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SI:BZ1G18.3.
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                                                                                    NCBI_TaxID=4577;
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NCBI_TaxID=7955;
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Hartmann A., ., Goh C.-S.,
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l; Mismatches
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Teleostei; Ostariophysi
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P., Elliott C., Schulze-Lefert
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Simmons C.R.,
P., Panstruga
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Search completed: July 21, 2004, 17:08:21 Job time : 10.5203 secs
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specific seven transmembrane Mlo family.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029316; AAK88341.1; -.
GO; GO:0016021; Cintegral to membrane; IEA.
GO; GO:0008219; P:cell death; IEA.
InterPro; IPR004326; Mlo.
Pram; PP03094; Mlo; 1.
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NON TER 1
SEQUENCE 149 A
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STRAIN=ATCC 19718 / IFO 14298;

MEDLINE=22586410; PubMed=12700255;

MEDLINE=22586410; PubMed=12700255;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,

Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,

Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium and

obligate chemolithoautotroph Nitrosomonas europaea.";

J. Bacteriol. 185:2759-2773 (2003).

EMBL, BX321859; CAD84969.1;

EMBL, BX321859; CAD84969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. NE1058.
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                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 350 AA; 35890 MW; F33BB4F45BE1CA36 CRC64;
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Nitrosomonadaceae; Nitrosomonas.
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Last annotation update)
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